

GenCore version 5.1.6
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leic search, using sw model

April 12, 2004, 16:22:07 ; Search time 916.308 Seconds
(without alignments)

912.511 Million cell updates/sec

US-10-090-326-23

28
1 agcatcatctctgcatggtcagggtcat 28

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

27513289 seqs, 14931090276 residues

hits satisfying chosen parameters: 203984

length: 0
length: 60

: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_esta:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

is the number of results predicted by chance to have a
ater than or equal to the score of the result being printed,
rived by analysis of the total score distribution.

SUMMARIES

Query	Match	Length	DB	ID	Description
60.7	46	9	AV948819	AV948819	AV948819 AV948819
57.1	49	9	AI762609	AI762609	AI762609 w156d08.x
56.4	57	14	D71055	D71055	D71055 CELK061E3R
54.3	59	14	CB058981	CB058981	CB058981 NISC_jx10

60	10	AM458816	52.9	14.8	5
27	12	BM396377	52.1	14.6	6
49	9	AA515410	52.1	14.6	7
51	29	CC515838	51.4	14.4	8
55	28	BZ763116	51.4	14.4	9
36	28	AZ591147	50.7	14.2	10
39	28	AZ635338	50.7	14.2	11
50	28	AZ330881	50.7	14.2	12
58	9	AL651765	50.7	14.2	13
58	29	GGA320139	50.7	14.2	14
52	9	AA489521	50.0	14	15
52	9	AA492773	50.0	14	16
53	28	AZ922240	50.0	14	17
56	29	LBFA030DI2	50.0	14	18
50	14	AUI06538	49.3	13.8	19
51	19	CB260365	49.3	13.8	20
55	28	AZ789849	49.3	13.8	21
57	28	BH911716	49.3	13.8	22
59	29	CG869799	49.3	13.8	23
37	28	AZ824496	48.6	13.6	24
46	29	CG426656	48.6	13.6	25
49	9	AI670113	48.6	13.6	26
52	13	BQ086305	48.6	13.6	27
53	28	BZ661820	48.6	13.6	28
53	28	BZ661823	48.6	13.6	29
57	14	CB217728	48.6	13.6	30
58	9	AI952050	48.6	13.6	31
58	14	CA337713	48.6	13.6	32
59	14	CF842268	48.6	13.6	33
60	14	CD956570	48.6	13.6	34
30	28	AZ456409	47.9	13.4	35
31	28	BH906192	47.9	13.4	36
31	28	BH906199	47.9	13.4	37
42	29	AL765117	47.9	13.4	38
46	14	H92446	47.9	13.4	39
50	29	CC513990	47.9	13.4	40
55	9	AU014183	47.9	13.4	41
55	29	CG789246	47.9	13.4	42
29	14	CA797153	47.1	13.2	43
37	9	AI442882	47.1	13.2	44
39	28	AZ419652	47.1	13.2	45
41	13	CS2224	47.1	13.2	46
51	29	AL754099	47.1	13.2	47
52	29	AL943090	47.1	13.2	48
57	9	AL797516	47.1	13.2	49
57	28	CC056995	47.1	13.2	50
58	9	AA931854	47.1	13.2	51
32	14	RI5883	46.4	13	52
33	9	AU243251	46.4	13	53
40	9	AI377260	46.4	13	54
40	9	AV834452	46.4	13	55
41	28	BH848702	46.4	13	56
44	28	AZ430558	46.4	13	57
46	9	AI250491	46.4	13	58
50	9	AUI04937	46.4	13	59
50	9	AUI04938	46.4	13	60
50	9	AUI04939	46.4	13	61
50	9	AUI04940	46.4	13	62
50	9	AUI04941	46.4	13	63
50	9	AUI04943	46.4	13	64
50	29	BX892187	46.4	13	65
52	29	CG720139	46.4	13	66
53	9	AL958295	46.4	13	67
54	10	AW781356	46.4	13	68
55	14	AA917476	46.4	13	69
55	14	H44869	46.4	13	70
57	12	BM433543	46.4	13	71
58	29	CG714576	46.4	13	72
60	14	CF845319	46.4	13	73
37	9	AA647854	45.7	12.8	74
42	29	BX894509	45.7	12.8	75
46	9	AA932378	45.7	12.8	76
46	9	AA561123	45.7	12.8	77

45.7	46	29	BX649708	BX649708 Arabidops	c 151	12.2	43.6	49	9	AA387830	AA387830
45.7	51	14	CA335447	CA335447 NISC lt11	c 152	12.2	43.6	49	29	CNS07F1F	AL60789
45.7	53	9	AL870437	AL870437 Arabidops	c 153	12.2	43.6	50	9	AUI02476	AUI02476
45.7	53	14	CB409427	CB409427 NISC nc05	154	12.2	43.6	50	9	AUI02687	AUI02687
45.7	53	14	CB410615	CB410615 NISC nc12	155	12.2	43.6	50	9	AUI02688	AUI02688
45.7	54	14	CD029902	CD029902 NISC nc12	156	12.2	43.6	50	9	AUI02689	AUI02689
45.7	56	9	AV674710	AV674710 Arabidops	157	12.2	43.6	50	9	AUI02690	AUI02690
45.7	56	28	BH221475	BH221475 Arabidops	158	12.2	43.6	50	9	AUI02695	AUI02695
45.7	56	28	BH638481	BH638481 Arabidops	159	12.2	43.6	50	9	AUI02697	AUI02697
45.7	56	28	BH651948	BH651948 Arabidops	160	12.2	43.6	50	9	AUI02698	AUI02698
45.7	57	28	AZ915988	AZ915988 Arabidops	161	12.2	43.6	50	9	AUI02700	AUI02700
45.7	58	14	CA336852	CA336852 NISC lv06	c 162	12.2	43.6	50	9	AUI03187	AUI03187
45.7	60	14	CD948943	CD948943 NISC lv06	c 163	12.2	43.6	50	9	AUI04165	AUI04165
45.7	60	14	AZ800842	AZ800842 Arabidops	c 164	12.2	43.6	50	9	AUI06406	AUI06406
45.0	30	28	AZ800842	AZ800842 Arabidops	c 165	12.2	43.6	50	9	AUI06468	AUI06468
45.0	37	9	AI544907	AI544907 Arabidops	c 166	12.2	43.6	50	9	AUI06529	AUI06529
45.0	41	14	T54451	T54451 Arabidops	c 167	12.2	43.6	50	9	AUI06541	AUI06541
45.0	47	14	H55642	H55642 Arabidops	c 168	12.2	43.6	50	9	AUI06866	AUI06866
45.0	47	28	AZ797405	AZ797405 Arabidops	c 169	12.2	43.6	51	12	BG577901	BG577901
45.0	49	9	AI120408	AI120408 Arabidops	c 170	12.2	43.6	51	28	AZ309542	AZ309542
45.0	49	9	CG869123	CG869123 Arabidops	c 171	12.2	43.6	52	9	AI925247	AI925247
45.0	49	29	CG869123	CG869123 Arabidops	c 172	12.2	43.6	52	14	CB377176	CB377176
45.0	50	12	BM532066	BM532066 Arabidops	c 173	12.2	43.6	52	14	T74264	T74264
45.0	50	12	BM765480	BM765480 Arabidops	c 174	12.2	43.6	53	10	BF507141	BF507141
45.0	57	14	CA850749	CA850749 Arabidops	c 175	12.2	43.6	54	29	LBAP042D08	LBAP042D08
45.0	59	12	B036242	B036242 Arabidops	c 176	12.2	43.6	55	13	BQ254913	BQ254913
45.0	60	14	CF116097	CF116097 Arabidops	c 177	12.2	43.6	56	9	AA795227	AA795227
44.3	29	28	AZ847949	AZ847949 Arabidops	c 178	12.2	43.6	56	29	BI199129	BI199129
44.3	33	29	TA122E04P	TA122E04P Arabidops	c 179	12.2	43.6	57	28	BH905200	BH905200
44.3	35	14	N73542	N73542 Arabidops	c 180	12.2	43.6	58	9	AI657773	AI657773
44.3	36	28	CC057367	CC057367 Arabidops	c 181	12.2	43.6	58	9	AA542007	AA542007
44.3	38	28	AZ501000	AZ501000 Arabidops	c 182	12.2	43.6	58	13	BQ264668	BQ264668
44.3	38	29	BX534430	BX534430 Arabidops	c 183	12.2	43.6	58	14	H55568	H55568
44.3	39	29	BX893335	BX893335 Arabidops	c 184	12.2	43.6	58	28	AZ331561	AZ331561
44.3	44	9	AW063999	AW063999 Arabidops	c 185	12.2	43.6	59	29	TA31G03P	TA31G03P
44.3	46	28	AZ429958	AZ429958 Arabidops	c 186	12.2	43.6	60	12	BQ264424	BQ264424
44.3	46	28	AZ840663	AZ840663 Arabidops	c 187	12.2	43.6	60	13	BQ264650	BQ264650
44.3	47	14	T98319	T98319 Arabidops	c 188	12.2	43.6	60	13	BQ264651	BQ264651
44.3	48	12	BG684299	BG684299 Arabidops	c 189	12.2	43.6	60	28	AZ829601	AZ829601
44.3	48	29	AL944927	AL944927 Arabidops	c 190	12.2	43.6	60	28	AZ829601	AZ829601
44.3	50	9	AUI02400	AUI02400 Arabidops	c 191	12.2	43.6	60	28	AZ829601	AZ829601
44.3	50	12	BG405996	BG405996 Arabidops	c 192	12.2	43.6	60	28	AZ829601	AZ829601
44.3	52	10	BF643549	BF643549 Arabidops	c 193	12.2	43.6	60	28	AZ829601	AZ829601
44.3	52	14	CB219037	CB219037 Arabidops	c 194	12.2	43.6	60	28	AZ829601	AZ829601
44.3	52	14	CB219037	CB219037 Arabidops	c 195	12.2	43.6	60	28	AZ829601	AZ829601
44.3	52	14	CB219037	CB219037 Arabidops	c 196	12.2	43.6	60	28	AZ829601	AZ829601
44.3	52	14	CB219037	CB219037 Arabidops	c 197	12.2	43.6	60	28	AZ829601	AZ829601
44.3	53	28	BH862150	BH862150 Arabidops	c 198	12.2	43.6	60	28	AZ829601	AZ829601
44.3	53	28	BH862150	BH862150 Arabidops	c 199	12.2	43.6	60	28	AZ829601	AZ829601
44.3	55	14	CB217964	CB217964 Arabidops	c 200	12.2	43.6	60	28	AZ829601	AZ829601
44.3	56	28	AZ785606	AZ785606 Arabidops	c 201	12.2	43.6	60	28	AZ829601	AZ829601
44.3	57	14	CA335631	CA335631 Arabidops	c 202	12.2	43.6	60	28	AZ829601	AZ829601
44.3	57	28	CC459224	CC459224 Arabidops	c 203	12.2	43.6	60	28	AZ829601	AZ829601
44.3	58	9	AA288434	AA288434 Arabidops	c 204	12.2	43.6	60	28	AZ829601	AZ829601
44.3	58	9	AA541299	AA541299 Arabidops	c 205	12.2	43.6	60	28	AZ829601	AZ829601
44.3	59	14	CA337764	CA337764 Arabidops	c 206	12.2	43.6	60	28	AZ829601	AZ829601
44.3	59	28	AZ642800	AZ642800 Arabidops	c 207	12.2	43.6	60	28	AZ829601	AZ829601
44.3	60	12	BG272272	BG272272 Arabidops	c 208	12.2	43.6	60	28	AZ829601	AZ829601
44.3	60	29	BX534432	BX534432 Arabidops	c 209	12.2	43.6	60	28	AZ829601	AZ829601
44.3	60	29	BX534432	BX534432 Arabidops	c 210	12.2	43.6	60	28	AZ829601	AZ829601
43.6	34	29	CB887559	CB887559 Arabidops	c 211	12.2	43.6	60	28	AZ829601	AZ829601
43.6	37	9	AA913126	AA913126 Arabidops	c 212	12.2	43.6	60	28	AZ829601	AZ829601
43.6	37	9	AA958086	AA958086 Arabidops	c 213	12.2	43.6	60	28	AZ829601	AZ829601
43.6	37	28	BH790463	BH790463 Arabidops	c 214	12.2	43.6	60	28	AZ829601	AZ829601
43.6	39	9	AV834166	AV834166 Arabidops	c 215	12.2	43.6	60	28	AZ829601	AZ829601
43.6	40	9	AA958439	AA958439 Arabidops	c 216	12.2	43.6	60	28	AZ829601	AZ829601
43.6	40	9	AI796152	AI796152 Arabidops	c 217	12.2	43.6	60	28	AZ829601	AZ829601
43.6	40	9	AA575251	AA575251 Arabidops	c 218	12.2	43.6	60	28	AZ829601	AZ829601
43.6	40	12	BH821604	BH821604 Arabidops	c 219	12.2	43.6	60	28	AZ829601	AZ829601
43.6	43	9	AA328331	AA328331 Arabidops	c 220	12.2	43.6	60	28	AZ829601	AZ829601
43.6	45	28	CC049880	CC049880 Arabidops	c 221	12.2	43.6	60	28	AZ829601	AZ829601
43.6	45	28	CC049880	CC049880 Arabidops	c 222	12.2	43.6	60	28	AZ829601	AZ829601
43.6	46	9	AA902889	AA902889 Arabidops	c 223	12.2	43.6	60	28	AZ829601	AZ829601
43.6	47	29	TA77F02P	TA77F02P Arabidops	c 224	12.2	43.6	60	28	AZ829601	AZ829601

42.9	50	9	AUI02483	AUI02483	AUI02483	C 297	11.8	42.1	53	28	BH892483	BH89248
42.9	50	9	AUI04870	AUI04870	AUI04870	C 298	11.8	42.1	54	28	B34737	B34737
42.9	50	9	AUI05585	AUI05585	AUI05585	C 299	11.8	42.1	55	9	AI091130	AI091130
42.9	50	9	AUI05586	AUI05586	AUI05586	C 300	11.8	42.1	56	14	CH256599	CH256599
42.9	50	9	AUI06344	AUI06344	AUI06344	C 301	11.8	42.1	57	14	CH795292	CH795292
42.9	50	9	AUI06794	AUI06794	AUI06794	C 302	11.8	42.1	57	28	BH758271	BH75827
42.9	50	9	AUI06795	AUI06795	AUI06795	C 303	11.8	42.1	58	9	AA643598	AA643598
42.9	50	14	CA338100	CA338100	NISC_lw10	C 304	11.8	42.1	58	29	CG987730	CG98773
42.9	50	28	AZ332306	AZ332306	IM0060B18	C 305	11.8	42.1	60	9	AI047804	AI047804
42.9	51	13	BQ239145	BQ239145	TA05036F	C 306	11.8	42.1	60	28	AI906209	AI906209
42.9	51	29	CG718276	CG718276	1119052C1	C 307	11.8	42.1	60	28	CC200308	CC20030
42.9	52	9	AA208481	AA208481	mv85a07.r	C 308	11.6	41.4	23	28	AZ354268	AZ35426
42.9	52	9	AA274507	AA274507	v802402.r	C 309	11.6	41.4	25	28	AZ417175	AZ41717
42.9	52	10	BF643664	BF643664	NP007G12E	C 310	11.6	41.4	26	29	TA24G03P	TA24G03P
42.9	52	14	CB410529	CB410529	NISC_nc12	C 311	11.6	41.4	28	9	AA537024	AA537024
42.9	52	28	BZ662155	BZ662155	SALK_0256	C 312	11.6	41.4	32	14	T77145	T77145
42.9	53	28	AZ775134	AZ775134	2M00707L11	C 313	11.6	41.4	34	9	AA984692	AA984692
42.9	53	28	BZ662624	BZ662624	SALK_0261	C 314	11.6	41.4	34	9	AU268597	AU268597
42.9	54	14	CA337584	CA337584	NISC_lw03	C 315	11.6	41.4	36	28	AZ609522	AZ60952
42.9	54	28	AQ026226	AQ026226	1(3)07615	C 316	11.6	41.4	36	29	BX534333	BX53433
42.9	54	28	BH414183	BH414183	1007036G0	C 317	11.6	41.4	37	9	AA522819	AA522819
42.9	55	12	BG811905	BG811905	doc02a06	C 318	11.6	41.4	38	28	AZ758198	AZ75819
42.9	55	14	CD029926	CD029926	mgmk004XM	C 319	11.6	41.4	38	28	BH755666	BH75566
42.9	56	9	AL800323	AL800323	AL800323	C 320	11.6	41.4	40	9	AA642607	AA642607
42.9	56	14	CA337917	CA337917	NISC_lw08	C 321	11.6	41.4	40	9	AI041512	AI041512
42.9	56	14	CA337917	CA337917	NISC_lw08	C 322	11.6	41.4	40	9	AA579743	AA579743
42.9	57	10	AW641265	AW641265	cm05c05_w	C 323	11.6	41.4	40	28	AZ604737	AZ60473
42.9	57	28	BH805522	BH805522	1008061A0	C 324	11.6	41.4	40	28	BH902530	BH90253
42.9	57	28	BH906438	BH906438	SALK_0333	C 325	11.6	41.4	42	29	BX651245	BX65124
42.9	58	9	AA937412	AA937412	0103f05.s	C 326	11.6	41.4	43	9	AA862169	AA862169
42.9	58	9	AI147450	AI147450	Q961d11.r	C 327	11.6	41.4	43	28	AZ588360	AZ58836
42.9	58	28	AZ9222051	AZ9222051	HRC0C2D10	C 328	11.6	41.4	43	28	AZ875350	AZ87535
42.9	59	9	AA071902	AA071902	mm71e04.r	C 329	11.6	41.4	44	14	CA796716	CA79671
42.9	60	10	BF506850	BF506850	10J22P67	C 330	11.6	41.4	45	28	BH854731	BH85473
42.1	27	28	AZ626851	AZ626851	1M0467013	C 331	11.6	41.4	47	12	BQ064943	BQ06494
42.1	27	28	AZ632301	AZ632301	1M0486C23	C 332	11.6	41.4	47	14	CF337893	CF33789
42.1	28	28	AZ623171	AZ623171	1M0460003	C 333	11.6	41.4	47	28	AZ581261	AZ58126
42.1	31	10	BF685654	BF685654	602140521	C 334	11.6	41.4	47	28	AZ804115	AZ80411
42.1	31	28	AZ945327	AZ945327	2M0206J09	C 335	11.6	41.4	50	9	AUI04041	AUI04041
42.1	32	28	AZ859128	AZ859128	2M0164B12	C 336	11.6	41.4	50	9	AUI04761	AUI04761
42.1	32	28	AZ989961	AZ989961	2M0273D03	C 337	11.6	41.4	50	28	AUI08031	AUI08031
42.1	34	28	AZ309524	AZ309524	1M0013104	C 338	11.6	41.4	50	28	BH227672	BH22767
42.1	36	10	AW245681	AW245681	2822809.s	C 339	11.6	41.4	50	28	BH789906	BH78990
42.1	36	28	AZ627044	AZ627044	2M0103A13	C 340	11.6	41.4	50	28	CC024195	CC02419
42.1	40	9	AJ239824	AJ239824	AJ239824	C 341	11.6	41.4	51	29	AL944876	AL94487
42.1	44	9	AU264623	AU264623	AU264623	C 342	11.6	41.4	52	9	AI204024	AI204024
42.1	44	14	T69111	T69111	yc31h09.r1	C 343	11.6	41.4	52	9	AI332999	AI332999
42.1	46	14	CF291149	CF291149	14ROOT--0	C 344	11.6	41.4	52	10	BF633916	BF63391
42.1	46	28	AZ459047	AZ459047	1M0263F07	C 345	11.6	41.4	52	14	CB217552	CB21755
42.1	47	9	AV833049	AV833049	AV833049	C 346	11.6	41.4	52	14	R05651	R05651
42.1	47	29	BX659718	BX659718	Arabidops	C 347	11.6	41.4	52	14	T93299	T93299
42.1	48	28	BH847205	BH847205	SALK_0445	C 348	11.6	41.4	52	28	B36269	B36269
42.1	48	28	CC024575	CC024575	3591_l_3	C 349	11.6	41.4	52	28	BH814586	BH81458
42.1	48	29	TA254C04P	TA254C04P	bruce1	C 350	11.6	41.4	52	29	CG893337	CG89333
42.1	49	9	AA19129	AA19129	z34a10.r	C 351	11.6	41.4	53	10	BF507246	BF50724
42.1	49	28	AZ373724	AZ373724	1M0126C05	C 352	11.6	41.4	53	29	AL944410	AL94441
42.1	50	9	AUI04274	AUI04274	AUI04274	C 353	11.6	41.4	54	9	AI159446	AI159446
42.1	50	9	AUI06540	AUI06540	AUI06540	C 354	11.6	41.4	54	14	CF797539	CF79753
42.1	50	9	AUI07152	AUI07152	AUI07152	C 355	11.6	41.4	54	14	CF297053	CF29705
42.1	50	9	AUI07153	AUI07153	AUI07153	C 356	11.6	41.4	54	14	CF859400	CF85940
42.1	50	9	AUI07271	AUI07271	AUI07271	C 357	11.6	41.4	54	28	AZ416838	AZ41683
42.1	50	12	CG271710	CG271710	mai52e08.	C 358	11.6	41.4	54	29	CG869495	CG86949
42.1	50	29	CA93346	CA93346	CH240_327	C 359	11.6	41.4	55	9	AA915742	AA915742
42.1	51	12	BIS26968	BIS26968	602927158	C 360	11.6	41.4	55	9	AI808781	AI808781
42.1	51	29	CNS07FF3	CNS07FF3	Atropheles	C 361	11.6	41.4	55	9	AW104102	AW104102
42.1	52	9	AI973612	AI973612	sd07c05.y	C 362	11.6	41.4	55	12	BG607617	BG60761
42.1	52	10	BE316749	BE316749	NF066E04L	C 363	11.6	41.4	55	28	BH910678	BH91067
42.1	52	13	BQ570298	BQ570298	g1147f10.	C 364	11.6	41.4	56	12	BG160532	BG16053
42.1	52	14	CB056129	CB056129	NISC_jj13	C 365	11.6	41.4	56	13	BX732612	BX73261
42.1	52	28	AZ658081	AZ658081	1M0534I08	C 366	11.6	41.4	56	28	AZ633063	AZ63306
42.1	53	14	CF291128	CF291128	14ROOT--0	C 367	11.6	41.4	57	28	AZ434302	AZ43430
42.1	53	28	B06520	B06520	CSRL-81f2-u	C 368	11.6	41.4	57	28	BH640783	BH64078
42.1	53	28	B06520	B06520	CSRL-81f2-u	C 369	11.6	41.4	58	9	AA056749	AA056749

41.4	58	9	AI093609	AI093609 ou82d05.s	C 443	11.4	40.7	58	14	CF844186	CF844186
41.4	58	10	BE213008	BE213008 IPBrn0135	C 444	11.4	40.7	58	28	AZ592089	AZ592089
41.4	58	14	CB274168	CB274168 mai89f05.	C 445	11.4	40.7	58	29	CG869466	CG869466
41.4	58	18	BZ590895	BZ590895 3590.1.80	C 446	11.4	40.7	59	9	AL872973	AL872973
41.4	58	29	CC494133	CC494133 CH240.329	C 447	11.4	40.7	59	12	BI522115	BI522115
41.4	58	29	CG247451	CG247451 1119082E0	C 448	11.4	40.7	59	12	BM863229	BM863229
41.4	58	29	CG247451	CG247451 1119082E0	C 448	11.4	40.7	59	28	CC455113	CC455113
41.4	59	12	BG162461	BG162461 dfl5a08.y	C 449	11.4	40.7	59	28	CC455113	CC455113
41.4	59	14	CB218879	CB218879 NISC nb11	C 450	11.4	40.7	59	29	AU938470	AU938470
41.4	59	14	CB218879	CB218879 NISC nb11	C 451	11.4	40.7	60	9	AI308953	AI308953
41.4	59	29	BX656294	BX656294 Arabidops	C 452	11.4	40.7	60	14	T24473	T24473
41.4	59	29	CNS04589	AL275058 Tetradops	C 453	11.2	40.0	23	12	BM397206	BM397206
41.4	60	10	BF611841	BF611841 dfl5g07.y	C 454	11.2	40.0	24	28	AZ825913	AZ825913
41.4	60	12	BI941096	BI941096 dfl5c06.y	C 455	11.2	40.0	26	28	AZ441490	AZ441490
41.4	60	28	AZ507903	AZ507903 1M0349G13	C 456	11.2	40.0	29	28	BZ358973	BZ358973
41.4	60	28	BH770466	BH770466 1Mgtag23	C 457	11.2	40.0	30	28	AZ309878	AZ309878
41.4	60	29	CG986097	CG986097 CH240.156	C 458	11.2	40.0	30	28	AZ791321	AZ791321
41.4	60	29	BX003621	BX003621 Arabidops	C 459	11.2	40.0	33	29	AL945047	AL945047
41.4	60	29	AZ490638	AZ490638 1M0323B13	C 460	11.2	40.0	34	12	BM399526	BM399526
40.7	21	28	BX559720	BX559720 BX559720	C 461	11.2	40.0	34	28	AZ623317	AZ623317
40.7	24	13	BX559720	AZ471002 1M0285E03	C 462	11.2	40.0	34	28	BH865029	BH865029
40.7	24	28	AZ471002	AZ471002 1M0285E03	C 463	11.2	40.0	34	28	CC179479	CC179479
40.7	25	28	AZ840905	AZ840905 2M0138H09	C 464	11.2	40.0	37	28	BZ379866	BZ379866
40.7	28	9	AA641517	AA641517 nr62e09.s	C 465	11.2	40.0	37	29	DME547235	DME547235
40.7	29	14	CF298165	CF298165 7LEAF--01	C 466	11.2	40.0	39	12	BI223730	BI223730
40.7	31	9	AI188860	AI188860 qd27a10.x	C 467	11.2	40.0	39	14	U44319	U44319
40.7	31	12	BJ082844	BJ082844 BJ082844	C 468	11.2	40.0	39	28	BH907039	BH907039
40.7	31	14	U19678	U19678 DRU19678.2e	C 469	11.2	40.0	40	9	AA683589	AA683589
40.7	31	28	AZ592386	AZ592386 1M0403H15	C 470	11.2	40.0	40	9	AI020727	AI020727
40.7	32	28	BH862997	BH862997 SALK_0929	C 471	11.2	40.0	40	9	AI459438	AI459438
40.7	36	28	AZ511031	AZ511031 1M0355F20	C 472	11.2	40.0	40	9	AJ237265	AJ237265
40.7	38	9	AU052705	AU052705 AU052705	C 473	11.2	40.0	40	12	BJ066312	BJ066312
40.7	38	28	AZ799531	AZ799531 2M0057M04	C 474	11.2	40.0	40	28	AZ335887	AZ335887
40.7	39	28	AZ593237	AZ593237 1M0404D16	C 475	11.2	40.0	40	28	CC025427	CC025427
40.7	39	28	BZ352916	BZ352916 SALK_1194	C 476	11.2	40.0	41	28	AL766232	AL766232
40.7	40	9	AA912398	AA912398 ol99c11.s	C 477	11.2	40.0	42	28	AZ592676	AZ592676
40.7	40	9	AI356141	AI356141 qv52h04.x	C 478	11.2	40.0	43	9	AA663711	AA663711
40.7	41	14	R85401	R85401 vq22a03.s1	C 479	11.2	40.0	43	14	W62611	W62611
40.7	42	28	AZ762556	AZ762556 1M0557M01	C 480	11.2	40.0	43	29	AG206053	AG206053
40.7	42	28	CC178649	CC178649 RST188.Ba	C 481	11.2	40.0	43	29	BX891475	BX891475
40.7	43	28	CC455620	CC455620 SALK_0850	C 482	11.2	40.0	44	14	D67718	D67718
40.7	44	14	W25663	W25663 zc64e08.r1	C 483	11.2	40.0	44	14	H54222	H54222
40.7	44	28	AZ949937	AZ949937 2M0213F18	C 484	11.2	40.0	44	28	BH862713	BH862713
40.7	45	28	AZ307696	AZ307696 1M0009G04	C 485	11.2	40.0	45	10	BE382645	BE382645
40.7	46	9	AI580559	AI580559 tb70d01.x	C 486	11.2	40.0	45	29	BX002065	BX002065
40.7	46	9	AA531890	AA531890 TGEStz32	C 487	11.2	40.0	46	9	AI006918	AI006918
40.7	46	14	R78378	R78378 yi78d11.s1	C 488	11.2	40.0	46	9	AL585781	AL585781
40.7	48	14	T11101	T11101 hbc668.Huma	C 489	11.2	40.0	46	14	H72220	H72220
40.7	50	9	AU102283	AU102283 AU102283	C 490	11.2	40.0	46	14	R39433	R39433
40.7	50	9	AU103943	AU103943 AU103943	C 491	11.2	40.0	46	14	BH910965	BH910965
40.7	50	9	AU107115	AU107115 AU107115	C 492	11.2	40.0	47	14	CF330472	CF330472
40.7	50	29	BX660472	BX660472 Arabidops	C 493	11.2	40.0	47	29	CG780418	CG780418
40.7	51	14	CB212627	CB212627 OML02907	C 494	11.2	40.0	48	9	AA930873	AA930873
40.7	51	28	AZ812952	AZ812952 2M0080E01	C 495	11.2	40.0	48	9	AI172854	AI172854
40.7	52	10	BE321037	BE321037 NFO33H04r	C 496	11.2	40.0	48	9	AA386692	AA386692
40.7	52	12	BM023092	BM023092 ie79c01.x	C 497	11.2	40.0	48	28	AZ442808	AZ442808
40.7	52	13	BQ400170	BQ400170 NISC.mp07	C 498	11.2	40.0	48	28	CC249527	CC249527
40.7	52	14	CA334971	CA334971 NISC.lt04	C 499	11.2	40.0	49	14	CB277333	CB277333
40.7	52	14	H37883	H37883 yp57g06.r1	C 500	11.2	40.0	49	28	AZ601892	AZ601892
40.7	52	14	U38140	U38140 OSU38140.FD	C 501	11.2	40.0	49	29	AL751906	AL751906
40.7	52	28	AZ776478	AZ776478 2M0010E07	C 502	11.2	40.0	49	29	BX546641	BX546641
40.7	52	28	AZ802331	AZ802331 2M0061M08	C 503	11.2	40.0	50	9	AI102696	AI102696
40.7	53	14	CA833023	CA833023 MCT022H11	C 504	11.2	40.0	50	9	AU103188	AU103188
40.7	53	29	AG233518	AG233518 Lotus.cor	C 505	11.2	40.0	50	9	AU104211	AU104211
40.7	53	29	AL938469	AL938469 Arabidops	C 506	11.2	40.0	50	9	AU105637	AU105637
40.7	54	28	AZ306177	AZ306177 IM0007G11	C 507	11.2	40.0	50	9	AU106544	AU106544
40.7	55	9	AA995974	AA995974 os13e08.s	C 508	11.2	40.0	50	9	AU106786	AU106786
40.7	55	9	AA393943	AA393943 zt78a02.r	C 509	11.2	40.0	50	9	AU106790	AU106790
40.7	55	9	AA618428	AA618428 ng03f10.s	C 510	11.2	40.0	50	9	AU106791	AU106791
40.7	55	14	CH510375	CH510375 VVD177E01	C 511	11.2	40.0	50	9	AU107924	AU107924
40.7	57	14	H55330	H55330 CHR220269.C	C 512	11.2	40.0	50	9	AU107925	AU107925
40.7	57	28	AZ792680	AZ792680 2M0045118	C 513	11.2	40.0	50	9	AU107928	AU107928
40.7	57	28	BH856937	BH856937 SALK_0775	C 514	11.2	40.0	50	14	CA301862	CA301862
40.7	57	28	BZ762334	BZ762334 SALK_0994	C 515	11.2	40.0	50	14	CF063684	CF063684
40.7	58	9	AI331551	AI331551 fa94b12.y	C 515	11.2	40.0	50	14	CF063684	CF063684

40.0	50	28	BH65934	SALK_1001
40.0	51	9	AV841510	AV841510
40.0	51	14	CF216385	PT1314 HY
40.0	51	28	AZ950924	AM2015M07
40.0	52	9	AA024314	mE92B08.r
40.0	52	9	AX966148	OB14B11.s
40.0	52	9	AI960257	sgC18A01.y
40.0	52	9	AA498851	vI82G06.r
40.0	52	9	AA545281	vJ94A07.s
40.0	52	14	W90057	zhG9h10.r1
40.0	52	28	AZ419921	IM0196F07
40.0	52	28	CC055143	SALK_0857
40.0	53	12	BI175652	OSTR051P1
40.0	53	14	CB220472	IABO22D02
40.0	53	14	CB227518	IRU4OF12
40.0	53	14	CB857849	NISC na10
40.0	54	14	CB226319	LRT32H11
40.0	54	28	B01770	C SRL-140C10
40.0	55	9	AA915005	VZ10G09.x
40.0	55	9	AI864678	wG79H05.x
40.0	55	10	BF647754	NF01LE02E
40.0	55	10	AW167165	xq71h03.x
40.0	55	29	GG719625	ll19058P1
40.0	56	12	BI145657	AV833419
40.0	56	14	F31360	HSPD23589 H
40.0	56	14	R67248	Y131g11.r1
40.0	56	28	AZ820546	AM0092J07
40.0	56	28	BH614932	KG00927-5
40.0	56	28	BH637938	LO0801P80
40.0	57	28	AZ480952	IM0302P10
40.0	57	29	AG244752	Lotus cor
40.0	58	9	AA822006	VP25a10.r
40.0	58	9	AA855566	vW65h05.x
40.0	58	9	AA92660	vI77a04.r
40.0	58	12	BG939089	GM30C04.y
40.0	58	28	AZ808093	CH0071K23
40.0	59	29	CG727548	ll119095D0
40.0	59	10	BF532725	602074809
40.0	59	12	B1220561	602936031
40.0	59	14	H44232	YP04b06.r1
40.0	59	28	AZ962219	2M0230P19
40.0	59	29	CG672163	RN173 Ba
40.0	60	9	AA426872	vF21C02.s
40.0	60	10	BF537627	602054507
40.0	60	13	BQ754494	EBed01 SQ
40.0	60	14	H39339	DR19 IFNGam
40.0	60	28	AQ026349	I(3)neoS4
40.0	60	28	BZ291246	SALK_1200
40.0	60	28	BZ291251	SALK_1200
40.0	60	28	BZ291252	SALK_1200
40.0	60	29	AL757468	Arabidops
40.0	60	29	AZ941927	2M0201D24
39.3	26	28	AZ979003	2M0283E21
39.3	28	28	AZ467181	IM0278H19
39.3	31	28	BH910655	SALK_0609
39.3	31	29	CG719197	ll119056B0
39.3	32	12	BG109638	602280758
39.3	34	9	AI021283	uB07a06.r
39.3	34	29	AL770598	Arabidops
39.3	35	29	TA291H03Q	Al486659 T. brucei
39.3	38	10	BE534187	601232196
39.3	38	12	BM399369	5009-0-57
39.3	39	11	CNS09H9S	Single re
39.3	39	28	AZ595333	LM0407F23
39.3	39	28	BZ766341	SALK_1372
39.3	40	29	TA130E05P	Al464109 T. brucei
CF314873				
CC797671				
LA459866				
AA959528				
AT148664				
CA851888				
AZ495884				
CF318522				
AZ776549				
CG80630				
AZ611292				
AA916352				
AA956485				
UA4245				
AZ81071				
BH79171				
BZ76366				
CG71781				
AZ259675				
W36748				
BZ28844				
AUI03385				
AUI04910				
AUI04911	</			

C	735	10.8	38.6	44	28	CC144412
C	736	10.8	38.6	44	28	CC144419
C	737	10.8	38.6	44	29	TA348H11P
C	738	10.8	38.6	45	9	AU270182
C	739	10.8	38.6	45	12	BM280419
C	740	10.8	38.6	45	28	BH857245
C	741	10.8	38.6	46	9	AA828199
C	742	10.8	38.6	46	9	AA922868
C	743	10.8	38.6	46	9	AA954628
C	744	10.8	38.6	46	9	AI300677
C	745	10.8	38.6	46	12	BI083683
C	746	10.8	38.6	46	28	AZ493022
C	747	10.8	38.6	46	28	BH790453
C	748	10.8	38.6	46	28	BH917812
C	749	10.8	38.6	46	28	BZ770300
C	750	10.8	38.6	47	14	CA902582
C	751	10.8	38.6	47	28	AZ783792
C	752	10.8	38.6	47	28	BH856951
C	753	10.8	38.6	48	14	WI0946
C	754	10.8	38.6	48	28	AZ591909
C	755	10.8	38.6	49	9	AI1219230
C	756	10.8	38.6	49	9	AA152159
C	757	10.8	38.6	49	14	R31902
C	758	10.8	38.6	50	9	AL639988
C	759	10.8	38.6	50	9	AUI02847
C	760	10.8	38.6	50	9	AUI03228
C	761	10.8	38.6	50	9	AUI05098
C	762	10.8	38.6	50	9	AUI05098
C	763	10.8	38.6	50	9	AUI05696
C	764	10.8	38.6	50	9	AUI06030
C	765	10.8	38.6	50	9	AUI07576
C	766	10.8	38.6	50	9	AUI08030
C	767	10.8	38.6	50	28	AZ820525
C	768	10.8	38.6	50	28	HSMC39C08
C	769	10.8	38.6	51	28	BZ352902
C	770	10.8	38.6	51	28	BZ597074
C	771	10.8	38.6	51	28	BZ664263
C	772	10.8	38.6	52	9	AA645273
C	773	10.8	38.6	52	9	AA629105
C	774	10.8	38.6	52	9	AA782045
C	775	10.8	38.6	52	10	BE322502
C	776	10.8	38.6	52	28	BH231086
C	777	10.8	38.6	52	28	BH813576
C	778	10.8	38.6	52	28	CC248881
C	779	10.8	38.6	52	29	EX004460
C	780	10.8	38.6	53	9	AA145269
C	781	10.8	38.6	53	10	BF165945
C	782	10.8	38.6	53	14	CB829386
C	783	10.8	38.6	53	28	BA2022
C	784	10.8	38.6	54	9	AA918034
C	785	10.8	38.6	54	12	GF941427
C	786	10.8	38.6	54	14	CF370077
C	787	10.8	38.6	54	28	AF524294
C	788	10.8	38.6	54	28	AZ389494
C	789	10.8	38.6	54	28	AZ463659
C	790	10.8	38.6	54	28	AZ606644
C	791	10.8	38.6	54	28	B03173
C	792	10.8	38.6	55	12	BG811905
C	793	10.8	38.6	55	9	AA014981
C	794	10.8	38.6	55	9	AA882007
C	795	10.8	38.6	55	9	AJ534089
C	796	10.8	38.6	55	9	AA641823
C	797	10.8	38.6	55	9	AA625424
C	798	10.8	38.6	55	12	BG935978
C	799	10.8	38.6	55	14	H12458
C	800	10.8	38.6	55	28	AZ510157
C	801	10.8	38.6	55	28	BZ764382
C	802	10.8	38.6	56	14	

56	28	BH791923	BH791923	SALK_0620	C 881	10.6	37.9	25	29	CC885336
56	28	BZ761779	BZ761779	SALK_0812	C 882	10.6	37.9	26	28	AZ313876
56	28	BZ764389	BZ764389	SALK_1245	C 883	10.6	37.9	26	28	BH810744
56	28	CC060506	CC060506	EY03325-3	C 884	10.6	37.9	26	29	TA129A07P
56	28	BX655720	BX655720	Arabidops	C 885	10.6	37.9	28	9	AI471841
56	29	LBAPF031H02	BX544154	Leishmani	C 886	10.6	37.9	29	9	AU256137
57	9	AA989441	AA989441	aJ81n04.s	C 887	10.6	37.9	29	28	AZ309154
57	9	AL595919	AL595919	AL595919	C 888	10.6	37.9	30	12	BM395434
57	12	BG173482	BG173482	602335795	C 889	10.6	37.9	31	9	AA581300
57	14	D45775	D45775	HMG502987	C 890	10.6	37.9	31	28	AZ605943
57	28	AZ333311	AZ333311	1M0062P15	C 891	10.6	37.9	31	28	BZ381841
57	28	AZ640607	AZ640607	1M0502011	C 892	10.6	37.9	31	28	AZ948437
57	28	BZ761724	BZ761724	SALK_0751	C 893	10.6	37.9	32	28	AZ662474
57	29	CG733686	CG733686	1119158E0	C 894	10.6	37.9	32	28	BH854494
57	29	BX289656	BX289656	Arabidops	C 895	10.6	37.9	33	12	BM398846
57	29	BX894722	BX894722	Arabidops	C 896	10.6	37.9	33	14	H23694
57	29	TA184E08P	AL474749	T. brucei	C 897	10.6	37.9	33	28	AZ363372
57	29	TA265D09P	AL484847	T. brucei	C 898	10.6	37.9	34	9	AA707825
58	9	AA706604	AA706604	ah26b04.s	C 899	10.6	37.9	34	9	AA436781
58	9	AI942620	AI942620	fc73f12.Y	C 900	10.6	37.9	34	28	AZ592538
58	9	AA253796	AA253796	mw05b01.r	C 901	10.6	37.9	35	28	AZ821491
58	9	AA620451	AA620451	ae58d02.s	C 902	10.6	37.9	35	28	AZ838284
58	10	BZ122763	BZ122763	23_07rev	C 903	10.6	37.9	35	28	AZ938626
58	13	BQ590752	BQ590752	E012599-0	C 904	10.6	37.9	35	28	CC053541
58	13	H0784137	H0784137	in10g04.Y	C 905	10.6	37.9	36	10	AW247788
58	14	R68613	R68613	Y106b11.bl	C 906	10.6	37.9	36	28	AZ338246
59	9	AA666844	AA666844	vm65g11.s	C 907	10.6	37.9	36	28	AZ354561
59	12	BG315025	BG315025	OP3_0.127	C 908	10.6	37.9	36	28	AZ486331
59	12	BQ551355	BQ551355	sad37a01..	C 909	10.6	37.9	36	28	AZ491747
59	13	BQ270424	BQ270424	ik10h06.Y	C 910	10.6	37.9	36	28	BH906165
59	14	CD007347	CD007347	VVB076508	C 911	10.6	37.9	36	29	TA61A06Q
59	14	CD0714565	CD0714565	VVB202D09	C 912	10.6	37.9	37	12	B1695409
59	14	CD716430	CD716430	VVB128E06	C 913	10.6	37.9	37	28	AZ838465
59	18	BH631194	BH631194	1007074G0	C 914	10.6	37.9	37	28	BZ598263
59	28	BX289623	BX289623	Arabidops	C 915	10.6	37.9	39	2	HSM010339
59	29	BX653271	BX653271	Arabidops	C 916	10.6	37.9	39	28	AZ828153
59	29	BX662691	BX662691	Arabidops	C 917	10.6	37.9	39	28	AZ948943
59	29	CNS040FI	AL268839	Tetraodon	C 918	10.6	37.9	39	29	CC800300
59	29	TA14208Q	AL268839	T. brucei	C 919	10.6	37.9	39	29	AG256137
59	29	TA232D07P	AL481048	T. brucei	C 920	10.6	37.9	40	9	AA029741
60	9	AA15453	AA15453	vc99b07.s	C 921	10.6	37.9	40	9	AA014602
60	12	B1793877	B1793877	ie3se11.Y	C 922	10.6	37.9	40	9	AI264704
60	12	BM529568	BM529568	fx64e10.Y	C 923	10.6	37.9	40	14	CAY96225
60	12	BM529744	BM529744	fx44e07.Y	C 924	10.6	37.9	40	14	H41025
60	12	BM530440	BM530440	fx25g08.Y	C 925	10.6	37.9	40	29	CG869712
60	12	BM530674	BM530674	fx47e10.Y	C 926	10.6	37.9	40	29	BX234325
60	12	BM532766	BM532766	fx45b10.Y	C 927	10.6	37.9	40	29	HSA247016
60	12	BM532801	BM532801	fx46f01.Y	C 928	10.6	37.9	41	12	B1819153
60	12	BM572474	BM572474	fx28d04.Y	C 929	10.6	37.9	41	14	R76301
60	12	BM858725	BM858725	fx78g12.Y	C 930	10.6	37.9	41	28	AZ596544
60	13	BQ127992	BQ127992	1j79h08.Y	C 931	10.6	37.9	41	28	AZ615427
60	13	BQ128109	BQ128109	1j81g02.Y	C 932	10.6	37.9	41	28	AZ848135
60	13	BQ130809	BQ130809	1j87h10.Y	C 933	10.6	37.9	41	28	AZ976999
60	13	BQ268119	BQ268119	1j95d10.Y	C 934	10.6	37.9	41	29	TA40D01Q
60	13	BQ268123	BQ268123	1j95e07.Y	C 935	10.6	37.9	42	13	CG621457
60	13	BQ268195	BQ268195	1j96d12.Y	C 936	10.6	37.9	42	29	CX79972
60	13	BQ610771	BQ610771	1l16a08.Y	C 937	10.6	37.9	43	9	AA906764
60	13	BQ707819	BQ707819	im39e02.Y	C 938	10.6	37.9	43	10	BE373472
60	13	BU789770	BU789770	ic42a04.Y	C 939	10.6	37.9	43	14	TI17570
60	13	BU948363	BU948363	lo50c01.Y	C 940	10.6	37.9	43	29	CG724749
60	14	CD713175	CD713175	VVB187A11	C 941	10.6	37.9	43	29	BX292057
60	14	CD963363	CD963363	SDU_100_G	C 942	10.6	37.9	44	28	AZ303870
60	14	HS2868	HS2868	EST002_Tes	C 943	10.6	37.9	44	28	AZ588580
60	28	AZ221949	AZ221949	HRCot1C11	C 944	10.6	37.9	44	28	AZ603654
60	28	BH799063	BH799063	1008114A0	C 945	10.6	37.9	45	14	H91384
60	28	BZ412803	BZ412803	XA016_Bay	C 946	10.6	37.9	45	28	AZ822654
60	29	CC883477	CC883477	SALK_0944	C 947	10.6	37.9	45	28	BZ763943
60	29	TA126803P	AL463818	T. brucei	C 948	10.6	37.9	45	28	BZ765959
19	28	AZ495849	AZ495849	1M0331N22	C 949	10.6	37.9	46	9	AI1131945
20	28	BZ387347	BZ387347	1M0346K12	C 950	10.6	37.9	46	9	AI188695
23	12	BM399459	BM399459	5009-0-57	C 951	10.6	37.9	46	9	AI300677
23	12	BM399514	BM399514	5009-0-58	C 952	10.6	37.9	46	9	AI941313
23	28	AZ849204	AZ849204	2M0150J02	C 953	10.6	37.9	46	9	AA485011

37.9 46 10 AM672631
37.9 46 14 R89440
37.9 46 14 T80129
37.9 46 28 A2990941
37.9 46 28 B2764482
37.9 48 9 A1568232
37.9 48 9 AV844988
37.9 48 28 A2452059
37.9 48 28 A2485287
37.9 48 28 B2383007
37.9 49 9 AA902559
37.9 49 12 B1315732
37.9 49 13 BQ101179
37.9 49 13 BQ548140
37.9 49 28 B2767173
37.9 50 9 AU102558
37.9 50 9 AU104700
37.9 50 9 AU104869
37.9 50 9 AU105640
37.9 50 9 AU105965
37.9 50 9 AU105967
37.9 50 9 AU106392
37.9 50 9 AU106561
37.9 50 28 AZ937712
37.9 50 28 BZ352480
37.9 50 28 BZ352482
37.9 50 28 BZ763937
37.9 51 13 BX722118
37.9 51 28 AZ760116
37.9 51 28 BH863979
37.9 51 28 AL763257
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37.9 52 9 AA856040
37.9 52 9 AA932205
37.9 52 9 A1089855
37.9 52 9 AAL70022
37.9 52 9 AU009185
37.9 52 10 BE321071
37.9 52 28 AZ796236
37.9 52 28 BH856416
37.9 52 28 BZ768008
37.9 53 9 AA846708
37.9 53 9 AL884376
37.9 53 9 AU258826
37.9 53 28 AZ623781
37.9 53 28 BH214712
37.9 53 28 BH902261

ALIGNMENTS

148819 46 bp mRNA linear EST 14-MAR-2002
148819 Nori Satoh unpublished cDNA library, egg Ciona
intestinalis cDNA clone cieg03p13 5', mRNA sequence.
148819
148819.1 GI:19426578

naa intestinalis
naa intestinalis
caryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
lebobranchia; Cionidae; Ciona.
(bases 1 to 46)
oh.N., Satou,Y., Kohara,Y. and Shin-i,T.
pressed genes in Ciona intestinalis
published (2000)
tact: Nori Satoh
partment of Zoology
ro University
kyo-Ku, Kyoto, Japan
1: 81-75-753-4081

AM672631 9A Explan
R89440 YQ05a01.r1
T80129 x17h02.s1
A2990941 2M0274E23
B2764482 SALK_1249
A1568232 tn67d03.x
AV844988 AV844988
AZ452059 IM0251P12
AZ485287 IM0312D07
BZ383007 SALK_1192
AA902559 o159b12.s
B1315732 saf78g09.
BQ101179 i125a03.y
BQ548140 rd20h05.y
BZ767173 SALK_1384
AU102558 AU102558
AU104700 AU104700
AU104869 AU104869
AU105640 AU105640
AU105965 AU105965
AU105967 AU105967
AU106392 AU106392
AU106561 AU106561
AZ937712 2M0196E01
BZ352480 SALK_0806
BZ352482 SALK_0806
BZ763937 SALK_1228
BX722118 BX722118
AZ760116 IM0553K04
BH863979 SALK_0950
AL763257 Arabidops
AL481361 T. brucei
AA856040 vW82a06.x
AA932205 om84g04.s
A1089855 Q320d06.x
AAL70022 m84b08.x
AU009185 AU009185
BE321071 NF033E04R
AZ796236 2M0051E21
BH856416 SALK_0797
BZ768008 SALK_1396
AA846708 a14b12.s
AU258826 AU258826
AZ623781 IM0461N17
BH214712 1006004C0
BH902261 SALK_0915

Fax: 81-75-705-1113
Email: satohascidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
1. 46
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="cieg03p13"
/tissue_type="whole animal"
/dev_stage="egg"
/clone_lib="Nori Satoh unpublished cDNA library"

ORIGIN

Query Match 60.7%; Score 17; DB 9; Length 46;
Best Local Similarity 76.9%; Pred. No. 1.5e+04;
Matches 20; Conservative 0; Mismatches 6; Indels 0;

QY 3 CATCATCTCTCGCATGTCAGGTTCAT 28
|||||

DB 33 CATCCCATCGCATGTCAGGTTCAT 8
|||||

RESULT 2

AI762609 49 bp mRNA linear EST
w156d08.x1 NCI CGAP Col6 Homo sapiens cDNA clone IMAGE:
similar to TR:Q90706 Q90706 CLE7. i, mRNA sequence.

AI762609
VERSION AI762609.1 GI:5178276

KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM

Homo sapiens
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho

REFERENCE
1 (bases 1 to 49)

AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE
National Cancer Institute, Cancer Genome Anatomy Projec

JOURNAL
Tumor Gene Index

COMMENT
Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmer

M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Greg Lennon, Ph.D.

Clone distribution: NCI-CGAP clone distribution inform

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert length: 1004 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality sequence stop: 1.

FEATURES

Location/Qualifiers
1. 49
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2394255"
/tissue_type="colon tumor, RER+"
/lab_host="DH108"
/clone_lib="NCI CGAP Col6"
/notes="Organ: colon; Vector: p77T3D-Pac (Pharm
modified polylinker; Site 1: Not 1; Site 2: Ec
Plasmid DNA from the normalized library NCI-CC
prepared, and ss circles were made in vitro. E
purification, this DNA was used as tracer in a
hybridization reaction. The driver was PCR-ampl
from a pool of 5,000 clones made from the same
cloneIDs 1057416-1061255, and 1144584-1145351
Subtraction by Bento Soares and M. Fatima Bone

ORIGIN

09:04:23 2004

us-10-090-326-23.max.rst

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57.1%; Score 16; DB 9; Length 49;
ilarity 79.2%; Pred. No. 3.8e+04;
Conservative 0; Mismatches 5; Indels 0; Gaps 0;

TCATCTCTGCATGTCAGGTC 26
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SCATTATCTGCATATTCAGGTC 27

55 57 bp mRNA linear EST 18-OCT-1999
061E3R Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
yo Caenorhabditis elegans cDNA clone yk61e3 3', mRNA sequence.
55 55.1 GI:11110762

orhabditis elegans
orhabditis elegans
ryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
ditodea; Rhabditidae; Peloderinae; Caenorhabditis.
bases 1 to 57)
ra,Y., Mitsuaki.H., Nishigaki,A., Motohashi,T., Sugimoto,A. and
rd an expression map of the C.elegans genome
ished (1994)
act: Yuji Kohara
me Biology Lab.
onal Institute of Genetics
1111, Mishima, Shizuoka 411, Japan
81-559-81-6854
81-559-81-6855
1: ykohara@lab.nig.ac.jp.
Location/Qualifiers
1. .57
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/clone="yk61e3"
/sex="hermaphrodite"
/dev_stage="embryo"
/clone_lib="Yuji Kohara unpublished cDNA:Strain N2
hermaphrodite embryo"

56.4%; Score 15.8; DB 14; Length 57;
ilarity 74.1%; Pred. No. 4.8e+04;
Conservative 0; Mismatches 7; Indels 0; Gaps 0;

TCATCTCTGCATGTCAGGTC 27
|||||
CATCTCTCCCATGTCAGGTC 7

38981 59 bp mRNA linear EST 17-JAN-2003
JX10d12.w1 Soares NMBPA Mus musculus cDNA clone IMAGE:5024687
mRNA sequence.
38981
38981.1 GI:27797268

musculus (house mouse)
musculus
aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
halia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
(bases 1 to 59)
CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
onal Cancer Institute, Cancer Genome Anatomy Project (CGAP),
or Gene Index
blished (1997)

Contact: Robert Strausberg, Ph.D.
Email: cgaps@mail.nih.gov
cDNA Library Preparation:
DNA Sequencing by: National Institutes of Health Intram
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution informa
found through the I.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
Plate: L1AM11070 row: G column: 24
Seq primer: T7 primer.
Location/Qualifiers
1. .59
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:5024687"
/tissue_type="pituitary gland"
/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Soares NMBPA"
/note="Organ: brain; Vector: pT7T3D-PacI; Site-
Site 2: EcoRI; 1st strand cDNA was primed with-
oligo(dT) primer
5'-AACGTGAAGATTCGCGCGCGTATCATGATTTT
double-stranded cDNA was ligated to EcoRI adapt
5'-AATTCGCGCAGAG-3' AND 5'-CCTCGTGGCG-3' (Pharm
digested with NotI and cloned into the NotI and
sites of the pT7T3D-PacI vector. Library went t
round of normalization, and was constructed in
laboratory of M. Bento Soares (University of Ic

Query Match 54.3%; Score 15.2; DB 14; Length 59;
Best Local Similarity 71.4%; Pred. No. 8.2e+04;
Matches 20; Conservative 0; Mismatches 8; Indels 0;

QY 1 AGCATCATCTCTCTGCATGTCAGGTCAT 28
|||||
Db 40 AGCAGGTGCTCTCTCGTGGTGGGTCCT 13

RESULT 5
AW458816 60 bp mRNA linear EST
LOCUS
DEFINITION
Gm-c1016-4807 5', mRNA sequence.
ACCESSION
AW458816
VERSION
AW458816.1 GI:7029033
KEYWORDS
SOURCE
ORGANISM
Glycine max (soybean)
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra
Spermatophyta; Magnoliophyta; eudicotyledons; core eudic
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; I
Glycine.
1 (bases 1 to 60)
Shoemaker,R., Keim,E., Vodkin,L., Erpelting,J., Coryell,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., M
Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., I
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Car
McCann,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108.
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Cor
```

09:04:23 2004

us-10-090-326-23.max.rst

h Memorial Parkway Huntsville, AL 35801 For further information
: (800)-533-4363 or contact via email: ccu@resgen.com
it Length: 272 Std Error: 0.00
primer: -40RP from Gibco.
Location/Qualifiers

1..60
/organism="Glycine max"
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/db_xref="taxon:3847"
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/tissue_type="immature flowers of field grown plants"
/lab_host="Xl10-Gold"
/clone_lib="Gm-cl016"
/note="Vector: pBluescript II XR; Site 1: EcoRI; Site 2:
XhoI. This cDNA library was constructed from mRNA isolated
from immature flowers of field grown plants. The cDNA
library was prepared using the Stratagene pBluescript II
XR library construction kit. Complementary DNA was
synthesized from mRNA using a primer consisting of a poly
(dT) sequence with a XhoI restriction site. EcoRI adapters
were ligated to the blunt-ended cDNA fragments followed by
XhoI digestion. The cDNA fragments were directionally
cloned into the EcoRI-XhoI restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into Xl10-Gold host cells. This library was
constructed by Dr. Randy Shoemaker and Dr. John
Expelding."

52.9%; Score 14.8; DB 10; Length 60;
milarity 73.1%; Pred. No. 1.2e+05;
Conservative 0; Mismatches 7; Indels 0; Gaps 0;

ATCATCCTCTGCATGTCAGTCAT 28
|||||
ATCTACCTATGATGTTAAGTTAT 41

96377 27 bp mRNA linear EST 17-JAN-2002
9-0-21-F09.t.2 Chilcoat/Turkewitz cDNA (large fraction)
rahymena thermophila cDNA, mRNA sequence.

96377 GI:18196550

rahymena thermophila
rahymena thermophila
aryota; Alveolata; Ciliophora; Oligohymenophorea;
enostomatida; Tetrahymenina; Tetrahymena.
(bases 1 to 27)
kewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,
nkel, J. and Klobutcher, L.
from Tetrahymena thermophila, strain CU428.1, growing cells
ublished (2002)
tact: Turkewitz AP
ecular Genetics and Cell Biology
ersity of Chicago
) E. 58th Street, Chicago, IL 60637, USA
.: 773 702 4374
t: 773 702 3172
ail: apturkew@midway.uchicago.edu
I primer: T3.
Location/Qualifiers
1..27
/organism="Tetrahymena thermophila"
/mol_type="mRNA"
/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: Bluescript 2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

ORIGIN

Query Match 52.1%; Score 14.6; DB 12; Length 27;
Best Local Similarity 77.3%; Pred. No. 9.6e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0;

QY 2 GCATCATCCTCTGCATGTCAG 23

Db 23 GCGACATCCACNCGCTGTCAG 2

RESULT 7
AA515410/c

LOCUS
DEFINITION
AA515410 49 bp mRNA linear EST
nf69a09.s1 NCI CGAP Co3 Homo sapiens cDNA clone IMAGE:9;
similar to TR:G189049 G189049 NADH UBIQUINONE OXIDOREDU
SURUNIT ; mRNA sequence.

ACCESSION
VERSION
AA515410 GI:2255010

KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
EST.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho

REFERENCE
AUTHORS
TITLE
NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Projec
Tumor Gene Index
Unpublished (1997)

JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmer
M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequen
Clone distribution: NCI-CGAP clone distribution inform
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality

Insert Length: 1832 Std Error: 0.00

Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 1.

FEATURES
source

1..49
Location/Qualifiers
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/clone="IMAGE:925144"
/sex="pooled"
/tissue_type="colon"
/lab_host="DH10B"
/clone_lib="NCI CGAP Co3"
/notes="Vector: p773D-Pac (Pharmacia) with a p
polylinker; Site 1: Not I; Site 2: Eco RI; 1st
was prepared from 12 pooled bulk tumor samples
with a Not I - oligo(dT) primer. Double-stranc
ligated to Eco RI adaptors (Pharmacia), digest
I and cloned into the Not I and Eco RI sites c
modified p773 vector. Library went through or
normalization."

ORIGIN

Query Match 52.1%; Score 14.6; DB 9; Length 49;
Best Local Similarity 81.0%; Pred. No. 1.3e+05;
Matches 17; Conservative 0; Mismatches 4; Indels 0;

QY 7 ATCTCTGCATGTCAGTCA 27

Db 44 ATCTCTGCATGTCAGTCA 24

5838 0_361A18.T7 CHORI-240 linear DNA GSS 17-JUN-2003
mic survey sequence.
5838 5838.1 GI:31834126
taurus (cow)
ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
alia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
dae; Bovinae; Bos.
bases 1 to 51)
.R., Cloutier, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L.,
.M., Scott, A., Lee, D., Girm, N., Olson, T., Mayo, M.,
erfield, Y., Kirpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R.,
ewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S.,
in, J., Marra, M., de Jong, P., McWilliam, S., Barris, W.,
ymple, P. P. and Tellam, R.
ne BAC End Sequences from Library CHORI-240, PLATES 294 to 398
ublished (2003)
x GSSs: CH240_361A18.TARBAC13P2
act: Rob Holt
encing
British Columbia Cancer Agency Genome Science Centre
W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
604-877-6085
604-877-6276
1: rhoit@bcgsc.ca
es are derived from the bovine BAC library CHORI-240
p://www.chori.org/bacpac/bovine240.htm). For BAC library
ability, please contact Pieter de Jong (pdejong@mail.cho.org).
es may be purchased from BACPAC Resources
p://www.chori.org/bacpac/ordering/information.html. This work
undertaken as part of the International Bovine BAC Mapping
ortium (IBBM) by CSIRO Livestock Industries, Australia and the
ish Columbia Genome Sciences Centre, Canada.
e: 361 row: A column: 18
primer: T7
s: BAC ends.
Location/Qualifiers
1..51
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_361A18"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
51.4%; Score 14.4; DB 29; Length 51;
ilarity 75.0%; Pred. No. 1.5e+05;
Conservative 0; Mismatches 6; Indels 0;
CATCATCTCTGCATGTCAGG 24
CATCATCTCTGCATGTCAGG 25
58316 55 bp DNA linear GSS 13-MAR-2003
X_113520.16.90.x Arabidopsis thaliana TDNA insertion lines
idopsis thaliana genomic clone SALK_113520.16.90.x, genomic
vey sequence.
58316 58316.1 GI:28935669

KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 55)
AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadriab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H.,
Shim, P., Zimmermann, J. and Ecker, J.R.
TITLE A Sequence-Indexed Library of Insertion Mutations in the
JOURNAL Arabidopsis Genome
COMMENT Unpublished (2001)
Contact: Joseph R. Ecker
The Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left bo
TDNA.
Class: TDNA tagged.
Location/Qualifiers
1..55
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_113520.16.90.x"
/clone_lib="Arabidopsis thaliana TDNA insertion
/note="PCR was performed on Arabidopsis thaliana
each of which contains one or more TDNA inser
elements. The resultant fragment for each line
directly sequenced to determine the genomic se
the site of insertion. Details of the protoc
be found at http://signal.salk.edu/tdna_protoc
ORIGIN
Query Match 51.4%; Score 14.4; DB 28; Length 55;
Best Local Similarity 75.0%; Pred. No. 1.6e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0;
QY 5 TCATCCTCTGCATGTCAGGTCAT 28
DB 30 TTATTTCTTCATGTCAGGACAT 53
RESULT 10
AZ591147 36 bp DNA linear GSS
LOCUS 1M0401D16F Mouse 10kb plasmid UUGC1M library Mus musculi
DEFINITION clone UUGC1M0401D16 F, genomic survey sequence.
ACCESSION AZ591147
VERSION AZ591147.1 GI:11713433
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 36)
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Har
Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausern, A. and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads fr
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 309, Biomedical Polymers Research Bldg., 20 S. 2030
84112, USA

801 585 5606
 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0491 row: D column: 16
 Seq primer: CGTTGTAACACGACGCCAGT
 s: plasmid ends
 quality sequence stop: 36.
 Location/Qualifiers

1. .36
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0401D16"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/) was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

50.7%; Score 14.2; DB 28; Length 36;
 nilarity 84.2%; Pred. No. 1.5e+05; Indels 0; Gaps 0;
 Conservative 0; Mismatches 3;

TCTGTCATGTCAGGTCA 27
 |||||
 TCTGAGGGTCAAGGCA 20

35338 39 bp DNA linear GSS 13-DEC-2000
 491E10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
 ne UUGC1M0491E10 R, genomic survey sequence.
 35338
 35338.1 GI:11757528

musculus (house mouse)
 musculus
 alyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 malia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 (bases 1 to 39)
 n.D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
 am, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 lly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 derhausen, A. and Wright, D., Weiss, R.
 se whole genome scaffolding with paired end reads from 10kb
 smid inserts
 ublished (2000)
 tact: Robert B. Weiss
 versity of Utah Genome Center
 .versity of Utah
 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 .12, USA

Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0491 row: E column: 10
 Seq primer: CACACAGAAACAGCTATGACC
 Class: plasmid ends
 High quality sequence stop: 39.
 Location/Qualifiers

1. .39
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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC1M0491E10"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant
 /clone_lib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PWD42nv; Purified genomic DNA fr
 musculus C57BL/6J (male) was obtained from the
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/)
 was hydrodynamically sheared by repeated passag
 0.005 inch orifice at constant velocity. The sh
 was blunt end-repaired with T4 DNA polymerase
 polynucleotide kinase. Adaptor oligonucleotide
 ligated to the blunt ends in high molar excess
 adaptor DNA was purified and size-selected fo
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from
 of pWD42 (gi|4732114|gb|AF129072.1), a copy-num
 inducible derivative of plasmid R1. The vector
 with adaptors complementary to the insert adapt
 purified. The sheared, adaptor mouse DNA was
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Strata
 and selected for ampicillin resistance."

ORIGIN

Query Match 50.7%; Score 14.2; DB 28; Length 39;
 Best Local Similarity 70.4%; Pred. No. 1.6e+05;
 Matches 19; Conservative 0; Mismatches 8; Indels 0;

QY 1 AGCATCATCTCTGCATGTCAGGTCA 27
 |||||
 Db 38 AGCAGCAGCAGCAGCAGGTGAGGCCA 12

RESULT 12
 AZ330881

LOCUS
 DEFINITION
 1M0056101R Mouse 10kb plasmid UUGC1M library Mus muscul
 clone UUGC1M0056101 R, genomic survey sequence.

ACCESSION
 AZ330881

VERSION
 AZ330881.1 GI:10393023

KEYWORDS
 GSS.

SOURCE
 Mus musculus (house mouse)

ORGANISM

Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mu
 1 (bases 1 to 50)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Ha
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausen, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads fr
 plasmid inserts

TITLE

JOURNAL

COMMENT

Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030
 84112, USA


```

801 585 5606
801 585 7177
l: dunn@genetics.utah.edu
rt Length: 10000 Std Error: 0.00
e: 0056 row: 1 column: 01
primer: CACACAGGAACAGCATGACCC
is: plasmid ends
quality sequence stop: 50.
Location/Qualifiers
1..50
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="CS7BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0056101"
/sex="Male"
/lab host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus CS7BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
50.7%; Score 14.2; DB 28; Length 50;
ilarity 70.4%; Pred. No. 1.8e+05;
Conservative 0; Mismatches 8; Indels 0; Gaps 0;
ATCATCTCTGCATGTCAGTCAT 28
|||||
AACACACTCTGCATGTTAAGATCCT 49

1765 XGC-gastrula Silurana tropicalis cDNA clone TGas036n10 5',
sequence.
1765
1765.1 GI:17662001

rana tropicalis (western clawed frog)
rana tropicalis
ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ybia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
podinae; Silurana.
(bases 1 to 58)
ing,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
fer Xenopus tropicalis EST project 2001 (11_2003)
blished (2003)
:act: Huckle E
per Institute
ton, Cambridgeshire, CB10 1SA, UK
l: trop@sanger.ac.uk
sequence is from a Xenopus Gene Collection (XGC) library
structed by Aaron M. Zorn.
was oligo dt primed from 5ug of poly A+ RNA from stages 10-13
:rules. EcoRI-NotI cut cDNA was then ligated into pCS107 with

```

```

EcoRI at the 5' end and NotI at the 3' end.
Vector: pCS107; Site 1: EcoRI; Site 2: NotI
Host: Escherichia coli XLI-blue
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE ID: TGas036n10.plkSP6
Sequencing primer: SP6
Location/Qualifiers
1..58
/organism="Silurana tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TGas036n10"
/dev_host="Gastrula (stages 10.5-12 mixed)"
/lab host="Escherichia coli XLI-blue"
/clone_lib="XGC-gastrula"
/note="Vector: pCS107; Site 1: EcoRI; Site 2: 1
was oligo dt primed from 5ug of poly A+ RNA fr
10-13 gastrulae. EcoRI-NotI cut cDNA was then
into pCS107 with EcoRI at the 5' end and NotI
end."

FEATURES
source
1..58
Query Match 50.7%; Score 14.2; DB 9; Length 58;
Best Local Similarity 84.2%; Pred. No. 1.9e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0;

QY 1 AGCATCATCTCTGCATGG 19
|||||
Db 49 AGCGCATCTCTTCATGG 31
|||||

RESULT 14
GGA320139/c 58 bp DNA linear GSS
LOCUS
Gallus gallus anonymous sequence from Cosmid mapping to
DEFINITION
microchromosome (Cosmid 32 - Contig 41), genomic survey
ACCESSION
AJ232043
VERSION
AJ232043.1 GI:3451861
KEYWORDS
GSS; genome survey sequence.
SOURCE
Gallus gallus
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 58)
Morris,J., Bruley,C.K., Paton,I.R., Dunn,I., Jones,C.T.,
Smith,J., Bruley,C.K., Law,A.S., Masabanda,J., Sazanov,A., Waddi
Pries,R. and Burt,D.W.
Differences in gene density on chicken macrochromosomes
microchromosomes
Anim. Genet. 31 (2), 96-103 (2000)
JOURNAL
MEDLINE
10782207
PUBMED
10782207
AUTHORS
Smith,J., Bruley,C.K., Paton,I.R., Law,A.S., Masabanda,J.
Waddington,D., Pries,R. and Burt,D.W.
Direct Submission
JOURNAL
Submitted (12-AUG-1998) Division of Molecular Biology, F
Institute, Roslin, Midlothian EH25 9PS, Scotland, UK
Location/Qualifiers
1..58
/organism="Gallus gallus"
/mol_type="genomic DNA"
/db_xref="taxon:9031"
/chromosome="microchromosome"

ORIGIN
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Best Local Similarity 84.2%; Pred. No. 1.9e+05;
Matches 16; Conservative 0; Mismatches 3; Indels 0;

QY 1 AGCATCATCTCTGCATGG 19
|||||

```

3CACACCCCTGCGATGG 1

89521 52 bp mRNA linear EST 11-AUG-1997
 lhl2.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone
 SE:843431 5' similar to SW:SPCN_CHICK P07751 SPECTRIN ALPHA
 IN, BRAIN ; mRNA sequence.

89521 89521

89521.1 GI:2219123

o sapiens (human)

o sapiens

aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 malia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 52)

lier L., Allen M., Bowles L., Dubuque T., Geisel G., Jost S.,
 aba T., Lacy M., Le N., Lennon G., Marra M., Martin J.,
 re B., Schellenberg K., Steptoe M., Tan F., Theising B.,
 te Y., Wylie T., Waterston R. and Wilson R.

hu-Merck EST Project 1997
 ublished (1997)

tact: Willson RK
 hington University School of Medicine

4 Forest Park Parkway, Box 8501, St. Louis, MO 63108

: 314 286 1800

: 314 286 1810

il: est@watson.wustl.edu

s clone is available royalty-free through LLNL ; contact the
 GE Consortium (info@image.llnl.gov) for further information.

ce considered overall poor quality
 sable reversed clone: similarity on wrong strand

primer: -28ml3 rev1 ET from Amersham
 h quality sequence stop: 1.

Location/Qualifiers
 1. .52

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:843431"

/sex="female"

/dev_stage="HeLa S3 cell line"

/lab_host="SOLR (kanamycin resistant)"

/clone_lib="Stratagene HeLa cell s3 937216"

/note=vector: pBluescript SK-; Site 1: EcoRI; Site 2:

XhoI; Cloned unidirectionally. Primer: Oligo dT. HeLa S3
 epitheloid carcinoma cells grown to semi-confluency
 without induction. Average insert size: 1.5 kb; Uni-ZAP XR
 Vector. -5' adaptor sequence: 5' GAATTCGCGACGAG 3' -3'
 adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

50.0%; Score 14; DB 9; Length 52;
 milarity 100.0%; Pred.No. 2.2e+05;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ATGGTCAGGTTCAT 28

|||||

ATGGTCAGGTTCAT 30

92773 52 bp mRNA linear EST 25-JUN-1997
 '609.r1 Stratagene mouse testis (#937308) Mus musculus cDNA
 ne IMAGE:918209 5' similar to SW:12A6 RAT P38062 INITIATION
 TOR 2 ASSOCIATED 67 KD GLYCOPROTEIN ; mRNA sequence.

92773 92773

92773.1 GI:2222335

; musculus (house mouse)

; musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mu
 1 (bases 1 to 52)

Marra M., Hillier L., Allen M., Bowles M., Dietrich N.,
 Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris

Schellenberg K., Steptoe M., Tan F., Underwood K., Moor
 Theising B., Wylie T., Lennon G., Soares B., Wilson R.

Waterston R.
 The WashU-HMI Mouse EST Project

Unpublished (1996)

Contact: Marra M/Mouse EST Project

WashU-HMI Mouse EST Project

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; con
 IMAGE Consortium (info@image.llnl.gov) for further info

MGI:530425

Trace considered overall poor quality
 Possible reversed clone: similarity on wrong strand

Seq primer: -28ml3 rev1 ET from Amersham
 High quality sequence stop: 1.

Location/Qualifiers
 1. .52

/organism="Mus musculus"

/mol_type="mRNA"

/strain="CD-1"

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/sex="males"

/tissue_type="testis"

/dev_stage="10-12 week old"

/lab_host="SOLR (kanamycin resistant)"

/clone_lib="Stratagene mouse testis (#937308)"
 /note="Organ: testis; Vector: pBluescript SK-;
 EcoRI; Site 2: XhoI; cloned unidirectionally.
 Oligo dT. Average insert size: 1.0 kb; Uni-ZAP
 -5' adaptor sequence: 5' GAATTCGCGACGAG 3' -3'
 sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

50.0%; Score 14; DB 9; Length 52;
 Best Local Similarity 77.3%; Pred.No. 2.2e+05;
 Matches 17; Conservative 0; Mismatches 5; Indels 0;

Qy 1 AGCATCATCTCTGCGATGGTCA 22

|||||

Db 25 AGCATCACCATCTCCATCTCA 4

|||||

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97346
tact: Peterson DG
nt Genome Mapping Laboratory
iversity of Georgia
n 162, Riverbend Research Bldg., 110 Riverbend Rd., Athens, GA
02, USA
: 706-583-0167
: 706-583-0160
il: dg@arches.uga.edu
ss: Hydroxyapatite-fractionated DNA.
Location/Qualifiers
1. .53
/organism="Sorghum bicolor"
/mol_type="genomic DNA"
/cultivar="BTx623"
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/dev_stage="seedling"
/clone_lib="Sorghum bicolor MRCoT"
/note="Vector: pGEM-TA-Easy; A Cot analysis was performed
for the sorghum genome. Based on the resulting Cot curve,
hydroxyapatite chromatography was used to isolate
'highly-repetitive' (HR), 'moderately-repetitive' (MR),
and 'single/low-copy' (SL) sequence components from
sheared genomic DNA. The three repetition-based DNA
components were cloned into E. coli to produce HRCot,
MRCoT, and SLCoT genomic libraries. Blotting and
sequencing data indicates that each library is
representative of the component from which it was derived.
Putative ID listings given for sequences are based on
comparison (blastn) with sequences in the NCBI Nr
Database. Only the primary match is given (all primary E
values are < or = 1.00E-5). In no instance does a 'Cot
clone' contain the complete sequence of its putative Nr
match."
Similarity 50.0%; Score 14; DB 28; Length 53;
Conservative 0; Mismatches 5; Indels 0; Gaps 0;
ATCATCTCTGCGATGGTCAGG 24
||||| |||||
TTTCATCTCAACATCGCCAGG 39
?030D12 56 bp DNA linear GSS 20-JUN-2003
shmania braziliensis GSS, clone LBAF030D12, genomic survey
ence.
i2120
i2120.1 GI:32136620
: Genomic survey sequence.
shmania braziliensis
shmania braziliensis
shmania braziliensis
shmania; Euglenozoa; Kinetoplastida; Trypanosomatidae;
shmania; Leishmania braziliensis species complex.
centino,E.C., Ruiz,J.C. and Cruz,A.K.
analysis of the Leishmania braziliensis genome
blished
(bases 1 to 56)
Z.A.K.
ect Submission
nted (17-JUN-2003) Cruz A.K., University of Sao Paulo,
artment of Molecular and Cell Biology, FMRP, Avenida
feirantes 3900, Ribeirao Preto, SP, 14049-900, BRAZIL
ne requests: akcruz@fmrp.usp.br.
Location/Qualifiers
1. .56
/organism="Leishmania braziliensis"
/mol_type="genomic DNA"

```

matophyta; Magnoliophyta; eudicotyledons; core eudicots;
 ids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 (bases 1 to 51)
 nid.K.J., Soerensen, T.R., Stracke, R., Torjek, O., Altmann, T.,
 chelli-Olas, T. and Weisshaar, B.
 ge-scale identification and analysis of genome-wide
 gle-nucleotide polymorphisms for mapping in Arabidopsis thaliana
 one Res. 13 (6), 1250-1257 (2003)

83290

99357

tact: Weisshaar B

S DNA core facility at MPZ

-Planck-Institute for Plant Breeding Research

1-von-Linne Weg 10, 50829 Koeln, Germany

il: 00492215062851

il: weisshaar@mpiz-koeln.mpg.de

ert Length: 51 Std Error: 0.00

te: 3 row: G column: 13

Primer: T7R; CTAATACGACTCACTATAGGA.

Location/Qualifiers

1. 51

/organism="Arabidopsis thaliana"

/mol_type="mRNA"

/cultivar="Niederzens-1 (Nd-1)"

/db_xref="GABI:588847"

/db_xref="taxon:3702"

/clone="MPZp770G133Q"

/tissue_type="whole plant"

/dev_stage="adult plant, mixed stresses"

/lab_host="E. coli TOP10"

/clone_lib="MPZ-ADIS-013"

/note="vector: pSPOR1; Site1: SalI; Site 2: NotI; RNA
 from total, adult, 6 weeks old Arabidopsis thaliana
 (accession Nd-1) plants, grown in the greenhouse under
 long day conditions in soil treated for 24 hours with
 different stresses, (1) at 4 Grad C in the dark, (2) at
 37 Grad C in the dark, (3) lying in the lab after removing
 from soil, (4) in the greenhouse after wounding with a
 forceps, (5) in the lab watering with a 150 mM NaCl
 solution, (6) at 26 Grad C in the light/UV; equal
 quantities of stressed plant material were pooled; library
 was made at the Max-Planck-Institute for Plant Breeding
 Research, Cologne, Germany; cloning sites SalI-NotI,
 primer sites and orientation:
 T7-SalI-CCACGCTCG-5prime-cDNA-polyA-CC-NotI-SP6; Note:
 Sequencing granted in the context of the GABI Arabidopsis
 Verbund I: Genetic Diversity, 'Establishment of
 high-efficiency SNP-based mapping tools and development of
 methods for genome-wide mutation detection' PI: Bernd
 Weisshaar Sequence submission managed by RZPD/GABI-Primary
 database: <http://gabi.rzpd.de>. This clone is available
 from RZPD; contact RZPD (clone@rzpd.de) for further
 information."

49.3%; Score 13.8; DB 14; Length 51;

milarity 72.0%; Pred. No. 2.6e+05;

Conservative 0; Mismatches 7; Indels 0; Gaps 0;

GCATCATCCCTCGTCAGTCAAGT 25

GGAGCATCGTTTCGTGTCAGT 20

'89849

103801F Mouse 10kb plasmid UUC1M library Mus musculus genomic

ne UUC2M0038H01 F, genomic survey sequence.

'89849

'89849.1 GI:12931098

; musculus (house mouse)

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mu
 1 (bases 1 to 55)

REFERENCE

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Ha
 Islan, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads fr

plasmid inserts

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss

University of Utah

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030

84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0038 row: H column: 01

Seq primer: CGTTGTAACGACGCGCCAGT

Class: plasmid ends

High quality sequence stop: 55.

FEATURES

source

1. 55

/organism="Mus musculus"

/mol_type="genomic DNA"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="UUC2M0038H01"

/sex="Male"

/lab_host="E. Coli strain XL10-Gold, Ti-resist
 /clone_lib="Mouse 10kb plasmid UUC1M library"
 /notes="Vector: PWD42nv; Purified genomic DNA f
 musculus C57BL/6J (male) was obtained from th
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares>
 was hydrodynamically sheared by repeated passa
 0.005 inch orifice at constant velocity. The s
 was blunt end-repaired with T4 DNA polymerase
 polynucleotide kinase. Adaptor oligonucleotide
 ligated to the blunt ends in high molar exces
 adapted DNA was purified and size-selected f
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from
 of pWD42 (GI4732114|GB|AF129072.1), a copy-nu
 inducible derivative of plasmid R1. The vector
 with adaptors complementary to the insert adap
 purified. The sheared, adapted mouse DNA was
 adapted vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Strata
 and selected for ampicillin resistance."

ORIGIN

Query Match 49.3%; Score 13.8; DB 28; Length 55;

Best Local Similarity 72.0%; Pred. No. 2.7e+05;

Matches 18; Conservative 0; Mismatches 7; Indels 0;

QY 3 CATCATCCCTCGTCAGTCAAGTCA 27

DB 37 CTTCATCCCTCGTTTGCACACTTA 13

RESULT 22

BH911716/c

LOCUS

BH911716 57 bp DNA linear GSS

DEFINITION

SALK_071735.19.20.x Arabidopsis thaliana TDNA insertion

Arabidopsis thaliana genomic clone SALK_071735.19.20.x,

survey sequence.

ACCESSION

BH911716

VERSION

BH911716.1

KEYWORDS

GSS.

oidopsis thaliana (thale cress)
oidopsis thaliana
aryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
matophyta; Magnoliophyta; eudicotyledons; core eudicots;
ids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
(bases 1 to 57)
nso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
rinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
nn,P., Zimmerman,J. and Ecker,J.R.
sequence-indexed Library of Insertion Mutations in the
bidopsis Genome
ublished (2001)
tact: Joseph R. Ecker
k Institute Genomic Analysis Laboratory (SIGnAL)
Salk Institute for Biological Studies
10 N. Torrey Pines Road, La Jolla, CA 92037, USA
: 858 453 4100 x1752
: 858 558 6379
il: ecker@salk.edu
s is single pass sequence recovered from the left border of
A. This sequence lies within 300 bases of the 3' end of
944560.
ss: TDNA tagged.

Location/Qualifiers
1. .57
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_071735.19.20.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

49.3%; Score 13.8; DB 28; Length 57;
milarity 72.0%; Pred. No. 2.7e+05;
Conservative 0; Mismatches 7; Indels 0; Gaps 0;

TGATCCTCTGCATGTCAGTGCAT 28
|||||
TTATTTCTACATGATTAGATCAT 18

69799 59 bp mRNA linear GSS 26-NOV-2003
931 Sanger Institute Gene Trap library pGT01xf Mus musculus
A, mRNA sequence.
69799
69799.1 GI:38533479

musculus (house mouse)
musculus
aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
malia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
(bases 1 to 59)
ger Intitute Gene Trap Resource.
p://www.sanger.ac.uk/PostGenomics/genetrap/
ublished (2003)
tact: Sanger Institute Gene Trap Resource
lcome Trust Sanger Institute
il: info.genetrap@sanger.ac.uk
uence tag generated by 5' RACE of total RNA from gene trap ES
1 line. ES cell lines harboring insertion mutation of target
e are available upon request from Sanger Institute Gene Trap
source. Annotation information available from
p://www.sanger.ac.uk/PostGenomics/genetrap/
ss: Gene Trap.

FEATURES

source
1. .59
Location/Qualifiers
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129 OLA"
/db_xref="taxon:10090"
/sex="Male"
/cell_type="Embryonic Stem Cell"
/clone_lib="Sanger Institute Gene Trap Library"
/notes="Vector: pGT01xf"

ORIGIN

Query Match 49.3%; Score 13.8; DB 29; Length 59;
Best Local Similarity 72.0%; Pred. No. 2.7e+05;
Matches 18; Conservative 0; Mismatches 7; Indels 0;

QY 2 GCATCATCTCTGCATGTCAGTGC 26
|||||

Db 49 GCATCATCTATATATGTCAGTGC 25
|||||

RESULT 24
AZ824496/c
LOCUS 37 bp DNA linear GSS
DEFINITION 2M0099C12F Mouse 10kb plasmid UUGC1M library Mus muscul
clone UUGC2M0099C12 F, genomic survey sequence.
ACCESSION AZ824496
VERSION AZ824496.1 GI:12994404
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mu
1 (bases 1 to 37)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Ha
Islan,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,
Reilly,M., Rose,M., Rose,R., Stokes,R., finge,A., von
Niederhauser,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads fr
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 203C
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0099 row: C column: 12
Seq primer: CGTTGTAAACGACGCGCCAGT
Class: plasmid ends
High quality sequence stop: 37.

FEATURES

source
1. .37
Location/Qualifiers
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0099C12"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resist
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA f
musculus C57BL/6J (male) was obtained from th
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares
was hydrodynamically sheared by repeated passa
0.005 inch orifice at constant velocity. The s
was blunt end-repaired with T4 DNA polymerase
polynucleotide kinase. Adaptor oligonucleotide
ligated to the blunt ends in high molar exce

adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (GI:4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RL. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

48.6%; Score 13.6; DB 28; Length 37;
 Similarity 80.0%; Pred. No. 2.6e+05;
 Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 SCATCATCTCTGCATGGT 20
 |||||
 SCACCTCCCTTCATGGT 1

26656 46 bp DNA linear GSS 15-SEP-2003
 0614-06A1-B06 UniformMu MutAIL Library Zea mays genomic clone
 0614-06A1-B06, genomic survey sequence.
 26656
 26656.1 GI:34735136

mays
 arysta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 rmatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 de; Panicoideae; Andropogoneae; Zea.
 (bases 1 to 46)
 Shaw, S., Tan, B.-C., Settles, A.M. and McCarty, D.R.
 uence tagged transposon insertions from the UniformMu maize
 ulation
 ublished (2003)
 tact: Donald R. McCarty
 nt Molecular and Cellular Biology Program
 versity of Florida
 110690 Gainesville, FL 32611-0690, USA
 : 352-392-1928 x322
 il: drmc@ufl.edu
 uence flanking probable Mu insertion site in UniformMu line:
 0614-06, Primer set: A
 ss: transposon insertion site.

Location/Qualifiers
 1. .46
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="W22 (ACR, bz1-m9)"
 /cultivar="UniformMu"
 /db_xref="taxon:4577"
 /clone="01S0614-06A1-B06"
 /clone_lib="UniformMu MutAIL Library"
 /note=Vector: TOPO-PCR4; DNA flanking Mu transposon
 insertions in Mu inactive lines were extracted from the
 UniformMu maize population by the thermo asymmetric
 interlaced PCR (TAIL) protocol using primers specific for
 the Mu terminal inverted repeat and a set of 16 arbitrary
 primers. Amplicons were size enriched using Sepharose 400
 spin columns and cloned into the TOPO PCR4 vector."

48.6%; Score 13.6; DB 29; Length 46;
 Similarity 67.9%; Pred. No. 2.9e+05;
 Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 AGCATCATCTCTGCATGGTCAGGTCAT 28
 |||||
 AGCAGCATCAAAAGCTTAGTGAGGTGAT 18

RESULT 26
 AI670113/c
 LOCUS
 DEFINITION

AI670113 49 bp mRNA linear EST
 wc11h10.x1 NCI CGAP Pr28 Homo sapiens cDNA clone IMAGE:
 similar to TR:Q61402 Q61402 GRANULE CELL ANTISERUM POSI
 mRNA sequence.

ACCESSION
 VERSION
 AI670113.1 GI:4834887
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM

REFERENCE
 1 (bases 1 to 49)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Projec
 Tumor Gene Index

Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D.,
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Sequencing by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequen
 Clone distribution: NCI-CGAP clone distribution inform
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Seq primer: -40UP from Gibco
 High quality sequence stop: 1..
 Location/Qualifiers
 1. .49
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2314915"
 /sex="male"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Pr28"
 /note=Organ: prostate; Vector: pT7T3D-Pac (Ph
 with a modified polylinker; Plasmid DNA from c
 normalized library NCI CGAP Pr22 was prepared,
 circles were made in vitro. Following HAP puri
 this DNA was used as tracer in a subtractive h
 reaction. The driver was PCR-amplified cDNAs f
 of 5,000 clones made from the same library (cl
 985608-986759, 110192-1101959, and 1217928-12
 Subtraction by Bento Soares and M. Fatima Bona

FEATURES
 source

ORIGIN

Query Match 48.6%; Score 13.6; DB 9; Length 49;
 Best Local Similarity 76.2%; Pred. No. 3e+05; Indels 0;
 Matches 16; Conservative 0; Mismatches 5;

QY 5 TCATCTCTCTGCATGGTCAGGT 25
 |||||

Db 49 TCATCATATGCATGTCAGGT 29
 |||||

RESULT 27

BQ086305/c
 LOCUS
 DEFINITION
 i21302.y1 Melton Normalized Human Islet 4 N4-HIS 1 Hom
 cDNA clone IMAGE:6135075 5', mRNA sequence.
 ACCESSION
 BQ086305
 VERSION
 BQ086305.1 GI:20045509
 EST.
 SOURCE
 Homo sapiens (human)

ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophytes; Magnoliophyta; eudicotyledons; core eudicotyledons; eurosids II; Brassicales; Brassicaceae; Arabidoideae; eurosid 1 (bases 1 to 53)

REFERENCE
AUTHORS Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
The Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu

TITLE This is single pass sequence recovered from the left bo TDNA. This sequence lies within an annotated exon of AT Class: TDNA tagged.

FEATURES
source
location/Qualifiers
1..53
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK_025297.38.35.x"
/clone_lib="Arabidopsis thaliana TDNA insertion"
note="PCR was performed on Arabidopsis thaliana each of which contains one or more TDNA insert elements. The resultant fragment for each line directly sequenced to determine the genomic se the site of insertion. Details of the protocol be found at http://signal.salk.edu/tdna_proto

ORIGIN

Query Match	48.6%;	Score 13.6;	DB 28;	Length 53;
Best Local Similarity	67.9%;	Pred. No. 3.1e+05;		
Matches	19;	Conservative	0;	Mismatches 9;
Indels				0;

Oy

```

1 AGCATATCTCTGTCATGCAGTCCAT 28
||||| ||||| ||||| ||||| |||||
29 AGCACAAACCTTGATTGTCAAGTCTT 2

```

Ddb

BZ661823	53 bp	DNA	linear	GSS
SALK_025300.44.70.x Arabidopsis thaliana TDNA insertion				
Arabidopsis thaliana genomic clone SALK_025300.44.70.x survey sequence.				
BZ661823				
BZ661823.1 GI:28174982				
GSS				
Arabidopsis thaliana (thale cress)				
Arabidopsis thaliana				
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophytes; Magnoliophyta; eudicotyledons; core eudicotyledons; eurosids II; Brassicales; Brassicaceae; Arabidoideae; eurosid 1 (bases 1 to 53)				
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Shinn,P., Zimmerman,J. and Ecker,J.R.				
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome				
Unpublished (2001)				
Contact: Joseph R. Ecker				
The Salk Institute Genomic Analysis Laboratory (SIGNAL)				
The Salk Institute for Biological Studies				
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA				
Tel: 858 453 4100 x1752				
Fax: 858 558 6379				

```

1: eckersalk.edu
is single pass sequence recovered from the left border of
. This sequence lies within an annotated exon of At2g16250.
s: TDNA tagged.
Location/Qualifiers
1..53
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="SALK 025300.44.70.x"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna\_protocols.html"

48.6%; Score 13.6; DB 28; Length 53;
ularity 67.9%; Pred. No. 3.1e+05;
Conservative 0; Mismatches 9; Indels 0; Gaps 0;

CATCATCTCTGATGGTGTGAT 28
CACAAACCTTTGATTGTGACGTCT 2

17728 57 bp mRNA linear EST 06-FEB-2003
rbo4f04.y1 COGENE 6E MAN Homo sapiens cDNA clone IMAGE:5795095
mRNA sequence.
17728
17728.1 GI:28265920
s sapiens (human)
s sapiens
aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
nalia; Eutheria; Primates; Catarhini; Hominidae; Homo.
(bases 1 to 57)
-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
tional Cancer Institute, Cancer Genome Anatomy Project (CGAP),
or Gene Index
blished (1997)
tact: Robert Strausberg, Ph.D.
il: cgaps-r@mail.nih.gov
A Library Prepared by: The I.M.A.G.E. Consortium/LLNL
NA Library Arrayed by: National Institutes of Health Intramural
uencing Center (NISC)
one distribution: NCI-CGAP clone distribution information can be
nd through the I.M.A.G.E. Consortium/LLNL at:
oimage.llnl.gov
te: LHAM12897 row: L column: 8
primer: M13RPI reverse primer (ABI).
Location/Qualifiers
1..57
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5795095"
/tissue_type="mandible, pooled"
/dev stage="embryo, 6 weeks postconception"
/lab_host="DH10B"
/clone_lib="COGENE 6E MAN"
/note="vector: pAMP1; cDNA primed using oligo-dT primer,
directionally cloned into UDG sites of pAMP1. Size
selected for insert sizes ranging from 0.2-2.0 kb.
Normalized to Cot5. Primary library, non-amplified.
Library constructed by M. Lovett. For more information on
this library, please contact R. Tidwell (Washington

```

```

University) or visit the COGENE website at
http://hg.wustl.edu/COGENE/."

ORIGIN
Query Match 48.6%; Score 13.6; DB 14; Length 57;
Best Local Similarity 80.0%; Pred. No. 3.2e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0;

QY 3 CATCATCTCTGATGGTGTCA 22
||||| ||| ||| ||| |||
Db 1 CATCATCATCATCATCATCA 20

RESULT 31
AI952050/c
LOCUS
DEFINITION
AI952050 58 bp mRNA linear EST
wx45c12.x1 NCI CGAP Lu28 Homo sapiens cDNA clone IMAGE:
similar to SW:NP11 HUMAN P55209 NUCLEOSOME ASSEMBLY PRO
1.. mRNA sequence.

ACCESSION AI952050
VERSION AI952050.1 GI:5744360
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut;
Mammalia; Eutheria; Primates; Catarhini; Hominidae; Hor
1 (bases 1 to 58)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Pra
I.M.A.G.E. Consortium DNA Sequencing by: Washington Uni-
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution inform
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1521 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..58
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2546710"
/tissue_type="two pooled squamous cell carcino
/lab_host="DH10B"
/clone_lib="NCI-CGAP Lu28"
/note="Organ: lung; Vector: pCMV-SPORT6; Site
Site 2: NotI; Cloned unidirectionally. Primer
Library constructed by Life Technologies."

ORIGIN
Query Match 48.6%; Score 13.6; DB 9; Length 58;
Best Local Similarity 67.9%; Pred. No. 3.2e+05;
Matches 19; Conservative 0; Mismatches 9; Indels 0;

QY 1 AGCATCATCTCTGATGGTGTGATCAT 28
||||| ||| ||| ||| |||
Db 39 ATCCTTCCTTCTTAGATGGACATCAT 12

RESULT 32
CA337713
LOCUS
DEFINITION
AI952050 58 bp mRNA linear EST
NISC lw05c10.y1 COGENE 4PA1 Homo sapiens cDNA clone IMA
5', mRNA sequence.
CA337713
ACCESSION

```



```

Email: bmtylet@vt.edu
PCR Primers
  FORWARD: BK reverse primer
  BACKWARD: BK reverse primer
Plate: 019 row: B column: 01
Seq primer: BK reverse primer
High quality sequence stop: 59.
  Location/Qualifiers
    1..59
      /organism="Phytophthora sojae"
      /mol_type="mRNA"
      /db_xref="taxon:67593"
      /clone="SHB019B01"
      /tissue_type="mycelium"
      /cell_line="P6437"
      /dev_stage="48 hr. post infection stage"
      /lab_host="Soybean plant"
      /clone_lib="USDA-IFARS:Expression of Phytophth
genes during infection and propagation_sHB"
      /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2:

ORIGIN
Query Match          48.6%; Score 13.6; DB 14; Length 59;
Best Local Similarity 80.0%; Pred.No.3.3e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0;

QY      2  GCATCATCTCTGCATGGTC 21
          |||||
Db       38  GCATCATGTCGCATGGAC 57

RESULT 34
CD956570/c
LOCUS      CD956570          60 bp mRNA linear EST
DEFINITION SCE127 GeneTag2 Zea mays cDNA, mRNA sequence.
ACCESSION  CD956570
VERSION    CD956570.1 GI:32804334
KEYWORDS   EST.
SOURCE     Zea mays
           Zea mays
           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poace
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 60)
           Genoplatne.
           Genoplatne, a major partnership french program in plant
TITLE      Unpublished (2003)
JOURNAL    Contact: Genoplatne
COMMENT    Genoplatne
           93, rue Henri Rochefort 91025 EVRY CEDEX France
           Tel: 33 1 69 47 54 00
           Fax: 33 1 69 47 54 10
           This sequence has been generated in the framework of t[
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and http://genoplatne-info.inbio.gen.fr).
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56409 1 GI:10614630

musculus (house mouse)
musculus
aryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
malia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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derhausern,A. and Wright,D., Weiss,R.
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smid inserts
ublished (2000)
tact: Robert B. Weiss
ersity of Utah
ersity of Utah
308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
12, USA

: 801 585 5606
: 801 585 7177
il: ddunn@genetics.utah.edu
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(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid RL. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

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DEFINITION
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survey sequence.

ACCESSION
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VERSION
KEYWORDS
SOURCE
ORGANISM

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Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr
Spermatophyta; Magnoliophyta; eudicotyledons; core eudi
rosids; eurosids II; Brassicales; Brassicaceae; Arabid
1 (bases 1 to 31)

REFERENCE
AUTHORS
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H.,
Shinn,P., Zimmermann,J. and Ecker,J.R.

TITLE
A Sequence-Indexed Library of Insertion Mutations in th
Arabidopsis Genome
Unpublished (2001)

JOURNAL
COMMENT
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379

Email: ecker@salk.edu
This is single pass sequence recovered from the left bc
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the site of insertion. Details of the protoc
be found at http://signal.salk.edu/tdna_prot

ORIGIN

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Matches 17; Conservative 0; Mismatches 6; Indels 0;

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RESULT 37

BH906199/c
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DEFINITION
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survey sequence.

ACCESSION
BH906199 1 GI:22719132

VERSION
KEYWORDS
SOURCE
ORGANISM

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Arabidopsis thaliana
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudi
rosids; eurosids II; Brassicales; Brassicaceae; Arabid
1 (bases 1 to 31)

REFERENCE
AUTHORS
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.
Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H.,


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Search completed: April 12, 2004, 19:18:30
Job time : 1230.31 secs

GenCore version 5.1.6
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cleic search, using sw model

April 12, 2004, 16:42:59 ; Search time 21.8462 Seconds
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US-10-090-326-23

28
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IDENTITY NUC

Gapop 10.0 , Gapext 1.0

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hits satisfying chosen parameters: 874574

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Listing first 1000 summaries

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SUMMARIES

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45.7	25	1	US-08-495-741-47	Sequence 47, Appl	237	12.6	45.0	32	4	US-09-543-141-7	Sequence
45.7	25	3	US-08-062-023-47	Sequence 7, Appl	238	12.6	45.0	32	4	US-09-417-197-91	Sequence
45.7	25	4	US-09-787-628-7	Sequence 1221, App	239	12.6	45.0	33	4	US-08-368-803-21	Sequence
45.7	26	2	US-08-859-998-1221	Sequence 1221, App	240	12.6	45.0	36	2	US-08-578-066A-22	Sequence
45.7	26	4	US-09-225-928-1221	Sequence 1221, App	241	12.6	45.0	36	2	US-08-790-517-12	Sequence
45.7	26	4	US-09-225-201B-1221	Sequence 910, App	242	12.6	45.0	36	3	US-09-240-426-22	Sequence
45.7	27	3	US-08-985-162-910	Sequence 1054, App	243	12.6	45.0	36	3	US-09-219-932-18	Sequence
45.7	27	4	US-08-679-645-1054	Sequence 910, App	244	12.6	45.0	36	3		
45.7	27	4	US-09-401-063-910		245	12.6	45.0	36	3		
45.7	27	4			246	12.6	45.0	36	3		

45.0	36	3	US-09-271-778-9	Sequence 9, Appli	C 320	12.4	44.3	32	3	US-08-870-930-4	Sequenc
45.0	36	4	US-09-362-831-22	Sequence 22, Appl	C 321	12.4	44.3	32	3	US-08-887-421-99	Sequenc
45.0	36	4	US-09-788-871-9	Sequence 9, Appli	C 322	12.4	44.3	32	3	US-08-973-124-44	Sequenc
45.0	37	3	US-08-726-807B-25	Sequence 25, Appl	C 323	12.4	44.3	32	3	US-08-973-124-187	Sequenc
45.0	37	3	US-09-258-367-25	Sequence 25, Appl	C 324	12.4	44.3	32	3	US-09-364-902-2	Sequenc
45.0	37	3	US-09-546-550-25	Sequence 25, Appl	C 325	12.4	44.3	32	3	US-09-275-850-40	Sequenc
45.0	37	3	US-09-431-414-25	Sequence 25, Appl	C 326	12.4	44.3	32	3	US-08-952-793-65	Sequenc
45.0	37	3	US-09-225-670-25	Sequence 25, Appl	C 327	12.4	44.3	32	4	US-09-363-939A-2	Sequenc
45.0	37	4	US-09-431-349C-25	Sequence 25, Appl	C 328	12.4	44.3	32	4	US-09-163-025B-3	Sequenc
45.0	37	4	US-09-450-072-49	Sequence 49, Appl	C 329	12.4	44.3	32	4	US-09-254-968-136	Sequenc
45.0	37	4	US-09-351-348-49	Sequence 49, Appl	C 330	12.4	44.3	32	4	US-09-849-928-65	Sequenc
45.0	39	1	US-08-481-003-14	Sequence 14, Appl	C 331	12.4	44.3	32	4	US-10-037-282-3	Sequenc
45.0	39	1	US-08-485-598-14	Sequence 14, Appl	C 332	12.4	44.3	32	4	US-09-854-662-2	Sequenc
45.0	40	4	US-08-952-445-33	Sequence 33, Appl	C 333	12.4	44.3	32	5	PCT-US95-12401A-3	Sequenc
45.0	41	4	US-09-468-872-20	Sequence 20, Appl	C 334	12.4	44.3	32	5	PCT-US96-08014-44	Sequenc
45.0	43	4	US-09-136-421-1	Sequence 1, Appli	C 335	12.4	44.3	32	5	PCT-US96-08014-187	Sequenc
45.0	43	4	US-08-997-918-15	Sequence 15, Appl	C 336	12.4	44.3	32	5	PCT-US96-09455A-65	Sequenc
45.0	45	3	US-08-979-608A-30	Sequence 30, Appl	C 337	12.4	44.3	32	5	PCT-US96-09472-77	Sequenc
45.0	45	4	US-09-517-849-30	Sequence 30, Appl	C 338	12.4	44.3	32	5	PCT-US96-09537-2	Sequenc
45.0	45	4	US-09-616-289-30	Sequence 30, Appl	C 339	12.4	44.3	33	2	US-08-488-402A-2	Sequenc
45.0	46	4	US-09-522-732B-21	Sequence 21, Appl	C 340	12.4	44.3	33	2	US-08-484-552A-2	Sequenc
45.0	47	2	US-08-600-783-15	Sequence 15, Appl	C 341	12.4	44.3	33	5	PCT-US96-09472-2	Sequenc
45.0	47	4	US-09-422-978-83	Sequence 83, Appl	C 342	12.4	44.3	34	4	US-09-522-217-57	Sequenc
45.0	50	4	US-09-443-199C-905	Sequence 906, App	C 343	12.4	44.3	34	4	US-09-923-246-57	Sequenc
45.0	51	1	US-08-248-016-3	Sequence 3, Appli	C 344	12.4	44.3	34	4	US-10-295-723-57	Sequenc
45.0	51	1	US-08-451-501-3	Sequence 3, Appli	C 345	12.4	44.3	35	1	US-08-283-067-5	Sequenc
45.0	51	1	US-08-379-926A-2	Sequence 2, Appli	C 346	12.4	44.3	35	1	US-08-283-067-25	Sequenc
45.0	51	1	US-08-379-926A-3	Sequence 3, Appli	C 347	12.4	44.3	35	1	US-08-447-411-77	Sequenc
45.0	51	3	US-08-642-541-7	Sequence 7, Appli	C 348	12.4	44.3	35	3	US-09-232-479-2	Sequenc
45.0	51	3	US-09-260-889-7	Sequence 7, Appli	C 349	12.4	44.3	35	3	US-09-784-990-2	Sequenc
45.0	51	4	US-09-479-275-4	Sequence 4, Appli	C 350	12.4	44.3	38	2	US-08-640-732-12	Sequenc
45.0	51	5	PCT-US95-06761-3	Sequence 3, Appli	C 351	12.4	44.3	38	5	PCT-US94-12778-12	Sequenc
45.0	52	2	US-08-713-455A-2	Sequence 2, Appli	C 352	12.4	44.3	39	1	US-08-481-003-1	Sequenc
45.0	54	1	US-08-060-822A-16	Sequence 16, Appl	C 353	12.4	44.3	39	3	US-08-485-598-1	Sequenc
45.0	54	1	US-08-060-822A-17	Sequence 17, Appl	C 354	12.4	44.3	40	1	US-08-317-403A-5	Sequenc
45.0	54	5	PCT-US94-05257-16	Sequence 16, Appl	C 355	12.4	44.3	40	1	US-08-471-985A-5	Sequenc
45.0	54	5	PCT-US94-05257-17	Sequence 17, Appl	C 356	12.4	44.3	40	1	US-08-433-126A-4	Sequenc
44.3	22	3	US-08-882-046-18	Sequence 18, Appl	C 357	12.4	44.3	40	1	US-08-433-124A-4	Sequenc
44.3	22	3	US-08-882-046-83	Sequence 8, Appl	C 358	12.4	44.3	40	2	US-08-477-527A-4	Sequenc
44.3	29	1	US-08-538-875-3	Sequence 3, Appli	C 359	12.4	44.3	40	3	US-08-481-710-4	Sequenc
44.3	29	4	US-09-304-232-371	Sequence 371, App	C 360	12.4	44.3	40	3	US-08-976-413A-4	Sequenc
44.3	30	1	US-08-484-557C-55	Sequence 55, Appl	C 361	12.4	44.3	40	5	PCT-US95-12401A-5	Sequenc
44.3	30	1	US-08-487-426B-55	Sequence 55, Appl	C 362	12.4	44.3	40	5	PCT-US96-06059-4	Sequenc
44.3	30	2	US-08-487-720A-55	Sequence 55, Appl	C 363	12.4	44.3	40	5	PCT-US96-09537-4	Sequenc
44.3	30	3	US-09-258-797-74	Sequence 74, Appl	C 364	12.4	44.3	41	1	US-08-368-803-15	Sequenc
44.3	31	1	US-08-095-726-66	Sequence 66, Appl	C 365	12.4	44.3	41	2	US-08-578-096A-17	Sequenc
44.3	31	1	US-08-096-043-63	Sequence 63, Appl	C 366	12.4	44.3	41	3	US-08-790-517-18	Sequenc
44.3	31	1	US-08-096-623A-71	Sequence 71, Appl	C 367	12.4	44.3	41	3	US-09-240-426-17	Sequenc
44.3	31	2	US-08-205-304-4	Sequence 4, Appli	C 368	12.4	44.3	41	3	US-09-219-932-24	Sequenc
44.3	31	2	US-08-859-998-238	Sequence 238, App	C 369	12.4	44.3	41	4	US-09-362-831-28	Sequenc
44.3	31	4	US-09-225-928-238	Sequence 238, App	C 370	12.4	44.3	42	3	US-08-938-830-30	Sequenc
44.3	31	4	US-09-225-201B-238	Sequence 238, App	C 371	12.4	44.3	43	1	US-08-475-063-35	Sequenc
44.3	32	1	US-08-399-412A-5	Sequence 5, Appli	C 372	12.4	44.3	43	1	US-08-207-792-35	Sequenc
44.3	32	1	US-08-317-403A-3	Sequence 3, Appli	C 373	12.4	44.3	43	3	US-08-732-708C-9	Sequenc
44.3	32	1	US-08-384-708A-99	Sequence 99, Appl	C 374	12.4	44.3	43	4	US-09-232-946-1	Sequenc
44.3	32	1	US-08-471-985A-3	Sequence 3, Appli	C 375	12.4	44.3	46	1	US-08-095-726-42	Sequenc
44.3	32	1	US-08-458-423A-44	Sequence 44, Appl	C 376	12.4	44.3	46	1	US-08-096-043-39	Sequenc
44.3	32	1	US-08-458-424B-44	Sequence 44, Appl	C 377	12.4	44.3	46	1	US-08-093-577-35	Sequenc
44.3	32	1	US-08-472-255A-65	Sequence 65, Appl	C 378	12.4	44.3	46	1	US-08-096-623A-47	Sequenc
44.3	32	1	US-08-479-724A-65	Sequence 65, Appl	C 379	12.4	44.3	47	4	US-09-422-978-1386	Sequenc
44.3	32	1	US-08-447-169A-61	Sequence 61, Appl	C 380	12.4	44.3	47	4	US-09-422-978-1941	Sequenc
44.3	32	2	US-08-488-402A-77	Sequence 77, Appl	C 381	12.4	44.3	50	2	US-08-850-049-122	Sequenc
44.3	32	2	US-08-465-591A-2	Sequence 2, Appli	C 382	12.4	44.3	50	2	US-08-050-478-122	Sequenc
44.3	32	2	US-08-465-594A-2	Sequence 2, Appli	C 383	12.4	44.3	50	3	US-09-091-814-50	Sequenc
44.3	32	2	US-08-233-012C-61	Sequence 61, Appl	C 384	12.4	44.3	50	3	US-09-414-117-122	Sequenc
44.3	32	2	US-08-484-552A-77	Sequence 77, Appl	C 385	12.4	44.3	50	4	US-09-678-437-122	Sequenc
44.3	32	2	US-08-792-075-2	Sequence 2, Appli	C 386	12.4	44.3	50	4	US-09-613-263-13	Sequenc
44.3	32	2	US-08-477-527A-2	Sequence 2, Appli	C 387	12.4	44.3	51	4	US-09-068-740A-34	Sequenc
44.3	32	2	US-08-894-578-105	Sequence 105, App	C 388	12.4	44.3	51	4	US-09-640-198D-6	Sequenc
44.3	32	3	US-08-472-256B-65	Sequence 65, Appl	C 389	12.4	44.3	52	2	US-09-639-667-23	Sequenc
44.3	32	3	US-08-481-710-2	Sequence 2, Appli	C 390	12.4	44.3	52	2	US-08-829-876-68	Sequenc
44.3	32	3	US-09-046-247-4	Sequence 4, Appli	C 391	12.4	44.3	52	4	US-09-234-874A-68	Sequenc
44.3	32	3	US-09-023-228B-3	Sequence 3, Appli	C 392	12.4	44.3	52	4	US-09-234-873A-68	Sequenc

44.3	54	2	US-08-452-724A-15	Sequence 15, Appl	466	12.2	43.6	35	4	US-09-530-139-66	Sequenc
44.3	54	4	US-08-453-623-15	Sequence 15, Appl	c 467	12.2	43.6	35	5	PCT-US93-01009-21	Sequenc
44.3	56	3	US-09-091-814-49	Sequence 49, Appl	468	12.2	43.6	36	3	US-08-941-445A-2	Sequenc
44.3	58	3	US-09-214-278-28	Sequence 28, Appl	c 469	12.2	43.6	39	1	US-08-120-607A-5	Sequenc
44.3	58	4	US-09-895-722-28	Sequence 28, Appl	c 470	12.2	43.6	39	2	US-08-453-848-5	Sequenc
44.3	58	4	US-09-723-368-26	Sequence 26, Appl	c 471	12.2	43.6	39	3	US-09-169-027-5	Sequenc
44.3	60	1	US-08-036-555B-167	Sequence 167, App	c 472	12.2	43.6	39	4	US-09-545-481-6	Sequenc
44.3	60	1	US-08-469-569-167	Sequence 167, App	c 473	12.2	43.6	40	2	US-08-713-815A-6	Sequenc
44.3	60	1	US-08-249-322A-167	Sequence 167, App	c 474	12.2	43.6	40	4	US-09-918-696-45	Sequenc
44.3	60	1	US-08-469-526A-167	Sequence 167, App	c 475	12.2	43.6	40	4	US-09-918-696-46	Sequenc
44.3	60	2	US-08-734-519A-167	Sequence 167, App	476	12.2	43.6	40	5	PCT-US94-08052-9	Sequenc
44.3	60	2	US-08-469-660-167	Sequence 167, App	477	12.2	43.6	41	3	US-08-813-507-114	Sequenc
44.3	60	3	US-08-470-335-167	Sequence 167, App	478	12.2	43.6	41	4	US-09-464-453-114	Sequenc
44.3	60	3	US-08-735-021-167	Sequence 167, App	c 479	12.2	43.6	45	1	US-07-884-811-21	Sequenc
44.3	60	3	US-08-734-664A-167	Sequence 167, App	c 480	12.2	43.6	45	1	US-07-885-971-21	Sequenc
44.3	60	3	US-08-470-339-167	Sequence 167, App	c 481	12.2	43.6	45	1	US-08-087-783A-21	Sequenc
44.3	60	4	US-08-467-602-167	Sequence 167, App	c 482	12.2	43.6	45	1	US-08-194-088B-21	Sequenc
44.3	60	5	PCT-US94-05083C-163	Sequence 163, App	c 483	12.2	43.6	45	1	US-08-435-501-20	Sequenc
44.3	60	5	PCT-US95-06846A-167	Sequence 167, App	c 484	12.2	43.6	45	1	US-08-435-764-20	Sequenc
43.6	18	3	US-08-621-700-10	Sequence 10, Appl	c 485	12.2	43.6	45	1	US-08-792-078-20	Sequenc
43.6	18	4	US-08-929-940-10	Sequence 10, Appl	c 486	12.2	43.6	45	1	US-08-482-882-46	Sequenc
43.6	18	4	US-09-625-972-13	Sequence 13, Appl	c 487	12.2	43.6	45	1	US-08-483-389-46	Sequenc
43.6	18	5	PCT-US95-03940-10	Sequence 10, Appl	c 488	12.2	43.6	45	2	US-08-487-113D-46	Sequenc
43.6	19	4	US-09-672-717-147	Sequence 147, App	c 489	12.2	43.6	45	2	US-08-473-503-46	Sequenc
43.6	20	1	US-08-735-963-9	Sequence 9, Appli	c 490	12.2	43.6	45	2	US-08-194-087-21	Sequenc
43.6	20	2	US-09-105-057-9	Sequence 9, Appli	c 491	12.2	43.6	45	2	US-08-483-932-46	Sequenc
43.6	20	3	US-09-304-214-9	Sequence 9, Appli	c 492	12.2	43.6	45	2	US-08-720-420A-46	Sequenc
43.6	20	4	US-09-423-890-17	Sequence 17, Appl	c 493	12.2	43.6	45	3	US-08-714-017-46	Sequenc
43.6	20	4	US-09-198-452A-5100	Sequence 5100, Ap	c 494	12.2	43.6	45	3	US-08-475-680-46	Sequenc
43.6	21	3	US-08-757-223-3	Sequence 3, Appli	c 495	12.2	43.6	45	5	PCT-US93-04648-21	Sequenc
43.6	22	3	US-08-480-173A-3	Sequence 3, Appli	c 496	12.2	43.6	45	5	PCT-US93-04717-20	Sequenc
43.6	22	3	US-08-484-408A-3	Sequence 3, Appli	c 497	12.2	43.6	46	1	US-08-441-430-29	Sequenc
43.6	22	4	US-09-468-872-48	Sequence 48, Appl	c 498	12.2	43.6	46	3	US-09-357-541-5	Sequenc
43.6	23	3	US-09-357-541-7	Sequence 7, Appli	c 499	12.2	43.6	46	3	US-09-357-541-6	Sequenc
43.6	23	3	US-09-357-541-8	Sequence 8, Appli	c 500	12.2	43.6	47	4	US-09-422-978-891	Sequenc
43.6	25	4	US-09-398-858-29	Sequence 29, Appl	c 501	12.2	43.6	47	4	US-09-422-978-891	Sequenc
43.6	25	4	US-09-866-108A-12932	Sequence 12932, A	c 502	12.2	43.6	47	4	US-09-422-978-891	Sequenc
43.6	25	4	US-08-865-108A-12933	Sequence 12933, A	c 503	12.2	43.6	49	4	US-09-400-541-10	Sequenc
43.6	27	1	US-08-232-538-4	Sequence 4, Appli	c 504	12.2	43.6	49	4	US-09-899-999-10	Sequenc
43.6	27	1	US-08-786-164-4	Sequence 4, Appli	c 505	12.2	43.6	50	2	US-08-615-961-7	Sequenc
43.6	27	3	US-08-985-162-1169	Sequence 1169, Ap	c 506	12.2	43.6	50	4	US-09-627-562A-1	Sequenc
43.6	27	3	US-08-584-040-3177	Sequence 3177, Ap	c 507	12.2	43.6	50	4	US-08-912-378A-1	Sequenc
43.6	27	4	US-08-584-040-3456	Sequence 3456, Ap	c 508	12.2	43.6	51	4	US-08-218-369-5	Sequenc
43.6	27	4	US-08-584-040-4627	Sequence 4627, Ap	c 509	12.2	43.6	51	4	US-08-218-369-14	Sequenc
43.6	27	4	US-09-393-858-27	Sequence 27, Appl	c 510	12.2	43.6	51	4	US-09-443-199C-166	Sequenc
43.6	27	4	US-09-401-063-1169	Sequence 1169, Ap	c 511	12.2	43.6	51	4	US-09-443-199C-166	Sequenc
43.6	28	1	US-09-598-218-1	Sequence 1, Appli	c 512	12.2	43.6	51	4	US-09-904-599A-5	Sequenc
43.6	29	1	US-08-293-086-8	Sequence 8, Appli	c 513	12.2	43.6	51	5	PCT-US95-03742-5	Sequenc
43.6	29	1	US-08-244-938-8	Sequence 8, Appli	c 514	12.2	43.6	51	5	PCT-US95-03742-14	Sequenc
43.6	29	2	US-08-861-306-8	Sequence 8, Appli	c 515	12.2	43.6	51	5	PCT-US96-03916-25	Sequenc
43.6	29	2	US-08-468-037A-35	Sequence 35, Appl	c 516	12.2	43.6	52	3	US-09-081-702-14	Sequenc
43.6	29	2	US-08-471-973A-35	Sequence 35, Appl	c 517	12.2	43.6	52	4	US-08-956-171B-1925	Sequenc
43.6	29	2	US-08-465-880-16	Sequence 16, Appl	c 518	12.2	43.6	54	1	US-08-386-579-12	Sequenc
43.6	29	3	US-09-035-357-35	Sequence 35, Appl	c 519	12.2	43.6	54	1	US-08-665-055-6	Sequenc
43.6	29	3	US-09-016-520-17	Sequence 17, Appl	c 520	12.2	43.6	54	3	US-08-342-924-11	Sequenc
43.6	29	3	US-09-144-611-8	Sequence 8, Appli	c 521	12.2	43.6	54	3	US-08-342-924-18	Sequenc
43.6	29	3	US-09-130-973-17	Sequence 17, Appl	c 522	12.2	43.6	54	3	US-08-960-111-17	Sequenc
43.6	29	3	US-09-477-902-17	Sequence 17, Appl	c 523	12.2	43.6	54	3	US-08-960-111-20	Sequenc
43.6	29	4	US-09-453-514A-8	Sequence 8, Appli	c 524	12.2	43.6	54	3	US-09-326-840-6	Sequenc
43.6	29	4	US-08-135-202-35	Sequence 35, Appl	c 525	12.2	43.6	54	3	US-08-665-057-6	Sequenc
43.6	29	4	US-08-802-331-16	Sequence 16, Appl	c 526	12.2	43.6	54	3	US-09-490-774-17	Sequenc
43.6	29	4	US-09-389-283-35	Sequence 35, Appl	c 527	12.2	43.6	54	3	US-09-490-774-20	Sequenc
43.6	29	4	US-09-370-541-11	Sequence 11, Appl	c 528	12.2	43.6	54	4	US-08-239-931-3	Sequenc
43.6	32	4	US-09-354-231B-25	Sequence 25, Appl	c 529	12.2	43.6	54	4	US-09-191-468-17	Sequenc
43.6	32	4	US-09-128-602B-25	Sequence 25, Appl	c 530	12.2	43.6	54	4	US-09-892-058A-6	Sequenc
43.6	32	4	US-09-995-297-25	Sequence 25, Appl	c 531	12.2	43.6	54	5	PCT-US96-01807-12	Sequenc
43.6	33	1	US-08-463-224-61	Sequence 61, Appl	c 532	12.2	43.6	58	3	US-09-248-643-13	Sequenc
43.6	33	1	US-08-463-377-61	Sequence 61, Appl	c 533	12.2	43.6	58	4	US-09-591-025-7	Sequenc
43.6	33	2	US-08-232-478-18	Sequence 61, Appl	c 534	12.2	43.6	58	4	US-09-894-927B-7	Sequenc
43.6	34	3	US-09-785-055-18	Sequence 18, Appl	c 535	12.2	43.6	59	1	US-08-482-882-91	Sequenc
43.6	34	4	US-08-483-511-21	Sequence 21, Appl	c 536	12.2	43.6	59	1	US-08-270-805C-18	Sequenc
43.6	35	3	US-08-823-823-41	Sequence 41, Appl	c 537	12.2	43.6	59	1	US-08-483-389-91	Sequenc
43.6	35	4	US-09-823-823-41	Sequence 41, Appl	c 538	12.2	43.6	59	2	US-08-410-654B-18	Sequenc

43.6	59	2	US-08-474-851-18	Sequence 18, Appl	12	42.9	37	1	US-08-428-733A-7	Sequence
43.6	59	2	US-08-481-560-18	Sequence 18, Appl	12	42.9	37	1	US-08-428-733A-38	Sequence
43.6	59	2	US-08-487-113D-91	Sequence 91, Appl	12	42.9	37	1	US-08-428-733A-39	Sequence
43.6	59	2	US-08-473-503-91	Sequence 91, Appl	12	42.9	38	1	US-08-464-339A-5	Sequence
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43.6	59	2	US-08-720-420A-91	Sequence 91, Appl	12	42.9	38	3	US-08-329-892B-19	Sequence
43.6	59	3	US-08-714-017-91	Sequence 91, Appl	12	42.9	39	6	5233482-34	Patent No
43.6	59	3	US-08-475-680-91	Sequence 91, Appl	12	42.9	40	3	US-09-262-773-148	Sequence
43.6	59	3	US-08-643-810A-18	Sequence 18, Appl	12	42.9	40	3	US-09-306-998-28	Sequence
43.6	60	3	US-09-023-228B-117	Sequence 117, App	12	42.9	40	4	US-09-317-789-3	Sequence
43.6	60	4	US-09-163-025B-117	Sequence 117, App	12	42.9	42	1	US-08-168-917-23	Sequence
43.6	60	4	US-10-037-282-117	Sequence 117, App	12	42.9	42	2	US-08-460-510-23	Sequence
43.6	60	6	5194425-8	Patent No. 5194425	12	42.9	42	2	US-08-460-490-23	Sequence
42.9	20	3	US-08-765-340-67	Sequence 67, Appl	12	42.9	42	5	PCT-US92-00730-23	Sequence
42.9	20	4	US-09-705-267A-168	Sequence 168, App	12	42.9	42	5	PCT-US92-10430-18	Sequence
42.9	20	4	US-09-843-376-36	Sequence 36, Appl	12	42.9	43	3	US-08-732-708C-6	Sequence
42.9	21	2	US-08-117-952-402	Sequence 402, App	12	42.9	43	3	US-08-732-708C-16	Sequence
42.9	21	2	US-08-863-639A-45	Sequence 45, Appl	12	42.9	43	3	US-08-732-708C-17	Sequence
42.9	21	2	US-08-863-639A-49	Sequence 49, Appl	12	42.9	43	4	US-09-313-221A-8	Sequence
42.9	21	2	US-08-863-639A-82	Sequence 82, Appl	12	42.9	43	4	US-08-168-917-20	Sequence
42.9	21	2	US-08-863-639A-86	Sequence 86, Appl	12	42.9	45	1	US-08-168-917-22	Sequence
42.9	21	4	US-09-676-610B-8	Sequence 8, Appli	12	42.9	45	1	US-08-168-917-22	Sequence
42.9	21	4	US-09-422-978-10737	Sequence 10737, A	12	42.9	45	2	US-08-460-510-20	Sequence
42.9	23	2	US-08-955-138-22	Sequence 22, Appl	12	42.9	45	2	US-08-460-510-22	Sequence
42.9	23	4	US-09-504-132-16	Sequence 16, Appl	12	42.9	45	2	US-08-460-490-20	Sequence
42.9	24	2	US-08-763-762-2	Sequence 2, Appli	12	42.9	45	2	US-08-460-490-22	Sequence
42.9	24	2	US-08-859-998-877	Sequence 877, App	12	42.9	45	4	US-09-383-143-23	Sequence
42.9	24	3	US-09-123-012-2	Sequence 2, Appli	12	42.9	45	4	US-09-383-143-24	Sequence
42.9	24	4	US-09-225-928-877	Sequence 877, App	12	42.9	45	4	US-09-518-914-11	Sequence
42.9	24	4	US-09-608-730B-6	Sequence 6, Appli	12	42.9	45	5	PCT-US92-00730-20	Sequence
42.9	24	4	US-09-225-201B-877	Sequence 877, App	12	42.9	45	5	PCT-US92-00730-22	Sequence
42.9	25	3	US-08-513-974B-201	Sequence 201, App	12	42.9	45	5	PCT-US92-10430-15	Sequence
42.9	25	4	US-09-866-108A-14950	Sequence 14950, A	12	42.9	45	5	PCT-US92-10430-17	Sequence
42.9	25	4	US-09-866-108A-14951	Sequence 14951, A	12	42.9	46	2	US-08-596-387B-63	Sequence
42.9	25	4	US-09-866-108A-14952	Sequence 14952, A	12	42.9	46	2	US-08-596-387B-64	Sequence
42.9	25	4	US-09-866-108A-14953	Sequence 14953, A	12	42.9	46	4	US-09-067-615-63	Sequence
42.9	25	4	US-09-866-108A-14954	Sequence 14954, A	12	42.9	46	4	US-09-067-615-64	Sequence
42.9	25	4	US-09-866-108A-14955	Sequence 14955, A	12	42.9	46	5	PCT-US95-09816A-63	Sequence
42.9	27	3	US-08-325-428B-10	Sequence 10, Appl	12	42.9	46	5	PCT-US95-09816A-64	Sequence
42.9	27	3	US-08-585-162-1301	Sequence 1301, Ap	12	42.9	47	4	US-09-486-241-7	Sequence
42.9	27	4	US-08-584-040-3457	Sequence 3457, Ap	12	42.9	47	4	US-09-422-978-1615	Sequence
42.9	27	4	US-08-584-040-5230	Sequence 5230, Ap	12	42.9	47	4	US-09-422-978-3595	Sequence
42.9	27	4	US-09-401-063-1301	Sequence 1301, Ap	12	42.9	48	1	US-08-168-917-21	Sequence
42.9	29	4	US-08-845-381E-9	Sequence 9, Appli	12	42.9	48	2	US-08-460-510-21	Sequence
42.9	30	2	US-08-850-048-88	Sequence 88, Appl	12	42.9	48	2	US-08-460-490-21	Sequence
42.9	30	2	US-08-050-478-88	Sequence 88, Appl	12	42.9	48	5	PCT-US92-00730-21	Sequence
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42.9	30	4	US-09-678-437-88	Sequence 88, Appl	12	42.9	51	3	US-08-974-609-13	Sequence
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42.9	36	1	US-08-411-796-250	Sequence 250, App	12	42.9	60	4	US-09-344-002B-41	Sequence
42.9	36	3	US-09-382-616A-26	Sequence 26, Appl	12	42.9	60	4	US-09-559-565C-41	Sequence
42.9	36	3	US-09-382-616A-28	Sequence 28, Appl	12	42.9	60	4	US-09-693-350-41	Sequence
42.9	36	4	US-08-559-390-250	Sequence 250, App	12	42.9	60	4	US-08-845-381E-60	Sequence
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42.9	37	1	US-08-474-542A-234	Sequence 234, App	11.8	42.1	15	4	US-09-479-122-30	Sequence
42.9	37	1	US-08-457-648-234	Sequence 234, App	11.8	42.1	15	4	US-09-484-997-30	Sequence
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42.1	17	1	US-08-281-940-65	Sequence 65, Appl	c 763	11.8	42.1	33	2	US-08-474-851-38	Sequenc
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42.1	17	2	US-08-485-885-65	Sequence 65, Appl	c 767	11.8	42.1	33	4	US-09-475-460A-29	Sequenc
42.1	17	3	US-09-295-186-15	Sequence 15, Appl	c 768	11.8	42.1	33	4	US-09-748-061A-29	Sequenc
42.1	18	1	US-08-241-465B-16	Sequence 16, Appl	c 769	11.8	42.1	34	1	US-09-387-418A-4	Sequenc
42.1	18	3	US-09-339-933-26	Sequence 26, Appl	c 770	11.8	42.1	35	1	US-08-464-523B-17	Sequenc
42.1	18	4	US-09-303-069-22	Sequence 22, Appl	c 771	11.8	42.1	36	4	US-09-463-282B-25	Sequenc
42.1	19	1	US-08-127-954-30	Sequence 30, Appl	c 772	11.8	42.1	37	3	US-08-445-463B-35	Sequenc
42.1	19	1	US-08-379-078-708	Sequence 708, Appl	c 773	11.8	42.1	37	3	US-08-445-464C-35	Sequenc
42.1	19	2	US-08-538-711A-18	Sequence 18, Appl	c 774	11.8	42.1	37	4	US-08-044-857D-35	Sequenc
42.1	19	3	US-08-725-027-18	Sequence 18, Appl	c 775	11.8	42.1	37	5	PCT-US94-03437-35	Sequenc
42.1	19	4	US-07-974-409C-292	Sequence 292, App	c 776	11.8	42.1	38	2	US-08-419-075-23	Sequenc
42.1	19	4	US-09-052-753B-10	Sequence 10, Appl	c 777	11.8	42.1	39	4	US-09-586-536-3	Sequenc
42.1	19	4	US-09-542-552-18	Sequence 18, Appl	c 778	11.8	42.1	39	4	US-09-657-931A-14	Sequenc
42.1	19	5	PCT-US93-00977-292	Sequence 292, App	c 779	11.8	42.1	40	3	US-09-262-773-109	Sequenc
42.1	20	3	US-09-490-692-110	Sequence 110, App	c 780	11.8	42.1	40	3	US-09-060-299-277	Sequenc
42.1	20	4	US-09-780-175-83	Sequence 83, Appl	c 781	11.8	42.1	40	4	US-09-402-923A-277	Sequenc
42.1	20	4	US-09-658-688A-58	Sequence 58, Appl	c 782	11.8	42.1	41	1	US-08-525-654B-139	Sequenc
42.1	20	4	US-08-422-978-11766	Sequence 276, App	c 783	11.8	42.1	41	1	US-08-481-003-6	Sequenc
42.1	20	4	US-09-060-299-276	Sequence 276, App	c 784	11.8	42.1	41	3	US-08-485-598-6	Sequenc
42.1	20	4	US-09-402-923A-276	Sequence 276, App	c 785	11.8	42.1	42	1	US-08-281-940-62	Sequenc
42.1	20	4	US-10-027-983-56	Sequence 56, Appl	c 786	11.8	42.1	43	4	US-09-425-638A-127	Sequenc
42.1	20	6	5194428-8	Patent No. 5194428	c 787	11.8	42.1	43	4	US-09-543-004-127	Sequenc
42.1	20	6	5194428-9	Patent No. 5194428	c 788	11.8	42.1	47	1	US-08-458-084-13	Sequenc
42.1	21	4	US-09-780-175-4	Sequence 4, Appl	c 789	11.8	42.1	47	1	US-08-305-508-13	Sequenc
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42.1	22	3	US-08-750-232-26	Sequence 26, Appl	c 795	11.8	42.1	47	4	US-09-422-978-1774	Sequenc
42.1	22	3	US-08-750-232-60	Sequence 60, Appl	c 796	11.8	42.1	47	5	PCT-US95-02945-13	Sequenc
42.1	22	3	US-09-479-005A-1178	Sequence 1178, App	c 797	11.8	42.1	48	4	US-09-624-693A-25	Sequenc
42.1	22	5	PCT-US95-08604-26	Sequence 26, Appl	c 798	11.8	42.1	48	4	US-08-704-867A-6	Sequenc
42.1	22	5	PCT-US95-08606-26	Sequence 26, Appl	c 799	11.8	42.1	49	2	US-08-726-528A-7	Sequenc
42.1	22	5	PCT-US95-08606-60	Sequence 60, Appl	c 800	11.8	42.1	49	3	US-08-434-099A-12	Sequenc
42.1	23	3	US-08-749-527-3	Sequence 3, Appl	c 801	11.8	42.1	49	4	US-08-897-956A-30	Sequenc
42.1	24	4	US-09-463-702A-16	Sequence 16, Appl	c 802	11.8	42.1	51	4	US-09-443-199C-717	Sequenc
42.1	24	4	US-09-699-135-16	Sequence 16, Appl	c 803	11.8	42.1	53	3	US-08-818-112-146	Sequenc
42.1	25	4	US-09-866-108A-12930	Sequence 12930, A	c 804	11.8	42.1	53	4	US-08-818-111-141	Sequenc
42.1	25	4	US-09-866-108A-12931	Sequence 12931, A	c 805	11.8	42.1	53	4	US-09-056-556-146	Sequenc
42.1	26	3	US-08-643-704A-32	Sequence 32, Appl	c 806	11.8	42.1	53	4	US-09-056-556-205	Sequenc
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42.1	26	3	US-08-683-403-6	Sequence 6, Appl	c 808	11.8	42.1	53	4	US-09-072-596-200	Sequenc
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42.1	27	3	US-08-985-162-1395	Sequence 1395, App	c 810	11.8	42.1	53	4	US-09-072-596-146	Sequenc
42.1	27	4	US-08-584-040-480	Sequence 480, App	c 811	11.8	42.1	54	1	US-08-094-948A-3	Sequenc
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42.1	27	4	US-08-584-040-3280	Sequence 3280, App	c 813	11.8	42.1	54	5	PCT-US96-09319-3	Sequenc
42.1	27	4	US-08-584-040-4836	Sequence 4836, App	c 814	11.8	42.1	57	4	US-09-097-055B-44	Sequenc
42.1	27	4	US-09-401-063-1395	Sequence 1395, App	c 815	11.8	42.1	57	4	US-09-097-055B-46	Sequenc
42.1	28	3	US-08-623-326-19	Sequence 19, Appl	c 816	11.8	42.1	57	4	US-09-097-055B-50	Sequenc
42.1	28	4	US-08-325-426B-6	Sequence 6, Appl	c 817	11.8	42.1	58	2	US-09-674-677-8	Sequenc
42.1	30	1	US-08-480-547A-20	Sequence 20, Appl	c 818	11.8	42.1	59	2	US-08-929-967-13	Sequenc
42.1	30	1	US-08-250-847B-20	Sequence 20, Appl	c 819	11.8	42.1	59	3	US-09-097-767A-3	Sequenc
42.1	30	1	US-08-186-229-23	Sequence 23, Appl	c 820	11.8	42.1	59	3	US-09-202-976-5	Sequenc
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42.1	30	2	US-08-476-176B-35	Sequence 35, Appl	c 823	11.8	42.1	60	4	US-09-611-29	Sequenc
42.1	30	2	US-08-859-998-393	Sequence 393, App	c 824	11.8	42.1	60	4	US-09-180-245-74	Sequenc
42.1	30	3	US-08-464-410A-20	Sequence 20, Appl	c 825	11.6	41.4	18	4	US-09-422-978-11132	Sequenc
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41.4	24	2	US-08-466-103A-20	Sequence 20, Appl	C 912	11.6	41.4	38	1	US-08-373-124A-2344	Sequenc
41.4	24	4	US-09-582-224A-1	Sequence 22, Appl	C 913	11.6	41.4	38	1	US-08-435-628-297	Sequenc
41.4	25	3	US-08-943-731-229	Sequence 229, App	C 914	11.6	41.4	38	1	US-08-435-628-2102	Sequenc
41.4	25	4	US-09-866-108A-3098	Sequence 3098, Ap	C 915	11.6	41.4	38	1	US-08-435-628-2344	Sequenc
41.4	25	4	US-09-866-108A-3107	Sequence 3107, Ap	C 916	11.6	41.4	38	3	US-09-156-828B-31	Sequenc
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41.4	25	4	US-09-866-108A-11217	Sequence 11217, A	C 920	11.6	41.4	39	3	US-09-079-984A-6	Sequenc
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41.4	25	4	US-09-866-108A-11353	Sequence 11353, A	C 925	11.6	41.4	41	3	US-09-039-641-26	Sequenc
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41.4	30	2	US-08-468-352-58	Sequence 58, Appl	C 943	11.6	41.4	45	3	US-09-315-886C-17	Sequenc
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41.4	36	1	US-08-411-796-245	Sequence 245, App	C 955	11.6	41.4	50	1	US-08-207-901-63	Sequenc
41.4	36	1	US-08-411-796-247	Sequence 247, App	C 956	11.6	41.4	50	1	US-08-530-492-55	Sequenc
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41.4	36	2	US-08-292-620A-1343	Sequence 1343, Ap	C 958	11.6	41.4	50	2	US-08-449-045C-24	Sequenc
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41.4	36	2	US-08-595-684B-311	Sequence 311, App	C 960	11.6	41.4	50	3	US-08-435-605A-36	Sequenc
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41.4	36	2	US-08-585-684B-1124	Sequence 1124, Ap	C 963	11.6	41.4	51	1	US-08-450-246-40	Sequenc
41.4	36	2	US-08-921-382-7	Sequence 7, Appli	C 964	11.6	41.4	51	1	US-08-451-233-40	Sequenc
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41.4	36	3	US-08-471-039-247	Sequence 247, App	C 967	11.6	41.4	51	4	US-09-387-418A-3	Sequenc
41.4	36	3	US-08-071-845-506	Sequence 506, App	C 968	11.6	41.4	51	4	US-09-443-199C-487	Sequenc
41.4	36	3	US-09-071-845-1343	Sequence 1343, Ap	C 969	11.6	41.4	51	4	US-09-443-199C-488	Sequenc
41.4	36	3	US-09-071-845-1521	Sequence 1521, Ap	C 970	11.6	41.4	51	4	US-09-443-199C-488	Sequenc
41.4	36	3	US-09-038-073-311	Sequence 311, App	C 971	11.6	41.4	53	4	US-09-126-420A-27	Sequenc
41.4	36	3	US-09-038-073-352	Sequence 352, App	C 972	11.6	41.4	54	4	US-09-479-645A-165	Sequenc
41.4	36	3	US-09-038-073-1122	Sequence 1122, Ap	C 973	11.6	41.4	54	4	US-09-479-645A-196	Sequenc
41.4	36	3	US-09-038-073-1124	Sequence 1124, Ap	C 974	11.6	41.4	55	1	US-08-450-257-39	Sequenc
41.4	36	4	US-08-559-330-245	Sequence 245, App	C 975	11.6	41.4	55	1	US-08-450-246-39	Sequenc
41.4	36	4	US-08-559-330-247	Sequence 247, App	C 976	11.6	41.4	55	1	US-08-450-098-39	Sequenc

41.4 55 1 US-08-451-233-39 Sequence 39, Appl
 41.4 55 1 US-08-450-236-39 Sequence 39, Appl
 41.4 55 1 US-08-235-403-39 Sequence 39, Appl
 41.4 55 4 US-09-088-274-3 Sequence 3, Appl
 41.4 59 1 US-08-275-156-1 Sequence 1, Appl
 41.4 59 1 US-08-275-156-2 Sequence 1, Appl
 41.4 59 5 PCT-US95-03866-29 Sequence 29, Appl
 41.4 60 2 US-08-749-852-52 Sequence 52, Appl
 41.4 60 2 US-08-749-852-54 Sequence 54, Appl
 41.4 60 4 US-09-459-956-22 Sequence 22, Appl
 41.4 60 4 US-08-584-040-7291 Sequence 7291, Ap
 40.7 17 1 US-09-371-772B-3100 Sequence 3100, Ap
 40.7 17 1 US-08-758-306-1357 Sequence 1357, Ap
 40.7 18 3 US-08-665-253-40 Sequence 40, Appl
 40.7 18 3 US-08-762-500-40 Sequence 40, Appl
 40.7 18 3 US-09-339-993-24 Sequence 24, Appl
 40.7 18 4 US-09-423-744A-10 Sequence 10, Appl
 40.7 19 1 US-08-631-200-58 Sequence 58, Appl
 40.7 19 1 US-08-829-553-58 Sequence 58, Appl
 40.7 19 2 US-08-922-267A-58 Sequence 58, Appl
 40.7 19 2 US-08-936-707A-58 Sequence 58, Appl
 40.7 19 3 US-08-936-706A-58 Sequence 58, Appl
 40.7 19 3 US-09-248-203-58 Sequence 58, Appl
 40.7 19 3 US-09-406-071-58 Sequence 58, Appl

ALIGNMENTS

Application US/08325426B
 17535
 ORINATION:
 : FU, Jianlin
 : TAN, Boon-Huan
 : YAP, Eu-Hian
 : CHAN, Yow-Cheong
 : TAN, Yin-Hwee
 INVENTION: CDNA SEQUENCE OF DENGUE VIRUS SEROTYPE 1
 INVENTION: (SINGAPORE STRAIN)
 SEQUENCES: 25
 DENCE ADDRESS:
 8th FLOOR, 1100 NORTH GLEBE ROAD
 ARLINGTON
 VIRGINIA
 : USA
 201-4714
 READABLE FORM:
 TYPE: Floppy disk
 : IBM PC compatible
 : PC-DOS/MS-DOS
 : Patent in Release #1.0, Version #1.25 (EPO)
 APPLICATION DATA:
 FION NUMBER: US/08/325,426B
 DATE: 16-DEC-1994
 FOR SEQ ID NO: 7:
 CHARACTERISTICS:
 29 base pairs
 nucleic acid
 NNESS: single
 f: linear
 TYPE: DNA (genomic)
 -7
 57.1%; Score 16; DB 3; Length 29;
 79.2%; Pred. No. 4.4e+02;
 : Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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 ATCAGAATTCTCTGATGTCAGG 25

RESULT 2

US-08-819-458A-14/c
 ; Sequence 14, Application US/08819458A
 ; Patent No. 5891669
 ; GENERAL INFORMATION:
 ; APPLICANT: Jensen, Ejner B.
 ; APPLICANT: Cherry, Joel
 ; APPLICANT: Elrod, Susan L.
 ; TITLE OF INVENTION: Methods For Producing Polypeptides
 ; TITLE OF INVENTION: In Respiratory-Deficient Cells
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: No. 5891669o No. 5891669disk of No. 5891669th A
 ; STREET: 405 Lexington Avenue
 ; CITY: New York
 ; STATE: NY
 ; COUNTRY: U.S.A.
 ; ZIP: 10174
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/819,458A
 ; FILING DATE: 17-MAR-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lambiris, Elias J.
 ; REGISTRATION NUMBER: 33,728
 ; REFERENCE/DOCKET NUMBER: 5215.000-US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-867-0123
 ; TELEFAX: 212-878-9655
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 30 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-819-458A-14
 Query Match 55.7%; Score 15.6; DB 2; Length 30;
 Best Local Similarity 81.8%; Pred. No. 6.5e+02;
 Matches 18; Conservative 0; Mismatches 4; Indels 0.

QY 1 AGCATCATCTCTGATGTCAGGTC 22

Db 26 ATCGTCATCTCTGCTTCGTCA 5

RESULT 3

US-09-206-059-71
 ; Sequence 71, Application US/09206059
 ; Patent No. 6201104
 ; GENERAL INFORMATION:
 ; APPLICANT: MacDonald, Nicholas
 ; APPLICANT: Sim, Kim Lee
 ; TITLE OF INVENTION: Angiogenesis-Inhibiting Protein Binding Pept
 ; TITLE OF INVENTION: Proteins and Methods of Use
 ; FILE REFERENCE: 05213-0370
 ; CURRENT APPLICATION NUMBER: US/09/206,059
 ; CURRENT FILING DATE: 1998-12-04
 ; NUMBER OF SEQ ID NOS: 80
 ; SOFTWARE: Patentin Ver. 2.0
 ; SEQ ID NO 71
 ; LENGTH: 33
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:


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3E: CELL GENESYS, INC.
    322 LAKESIDE DRIVE
    FOSTER CITY
    CALIFORNIA
    : USA
    4404
READABLE FORM:
TYPE: Floppy disk
R: IBM PC compatible
NG SYSTEM: PC-DOS/MS-DOS
E: PatentIn Release #1.0, Version #1.25
PPLICATION DATA:
TION NUMBER: US/08/258,152
DATE: 10-JUN-1994
ICATION: 435
LICATION DATA:
TION NUMBER: US 08/076,299
DATE: 11-JUN-1993
AGENT INFORMATION:
KRUPEN, KAREN I.
ATION NUMBER: 34,647
TE/DOCKET NUMBER: CELL 13.1
NICATION INFORMATION:
NE: 415-358-9600 X131
: 415-349-7392
FOR SEQ ID NO: 14:
CHARACTERISTICS:
    26 base pairs
    nucleic acid
    DNES: single
Y: linear
TYPE: DNA (genomic)
14
    51.4%; Score 14.4; DB 1; Length 26;
    imilarity 75.0%; Pred. No. 2e+03; 6; Indels 0; Gaps 0;
    : Conservative 0; Mismatches 6; Indels 0; Gaps 0;
ICATCTCTGCATGGTCAGTCAAT 28
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ICACCTTCTCAAGTCAGATCTT 2
-14/c
Application US/08076299A
334256
DRMATION:
: FINER, MITCHELL H.
: ROBERTS, MARGO R.
: DULL, THOMAS J.
: ZSEBO, KRISTINA M.
: QIN, LU
INVENTION: METHOD FOR PRODUCTION OF HIGH TITER
INVENTION: VIRUS AND HIGH EFFICIENCY RETROVIRAL MEDIATED TRANSDUCTION
SEQUENCES: 30
DENCE ADDRESS:
SE: CELL GENESYS, INC.
    322 LAKESIDE DRIVE
    FOSTER CITY
    CALIFORNIA
    : USA
    4404
READABLE FORM:
TYPE: Floppy disk
R: IBM PC compatible
NG SYSTEM: PC-DOS/MS-DOS
E: PatentIn Release #1.0, Version #1.25
PPLICATION DATA:
TION NUMBER: US/08/076,299A
DATE: 11-JUN-1993
ICATION: 435

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: KRUPEN, KAREN I.
; REGISTRATION NUMBER: 34,647
; REFERENCE/DOCKET NUMBER: CELL 13.0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-358-9600 X131
; TELEFAX: 415-349-7392
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-076-299A-14
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Best Local Similarity 75.0%; Pred. No. 2e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0
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DB 25 TCACCTTCTCAAGTCAGATCTT 2
RESULT 9
US-08-438-582-14/c
; Sequence 14, Application US/08438582
; Patent No. 5858740
; GENERAL INFORMATION:
; APPLICANT: FINER, MITCHELL H.
; APPLICANT: ROBERTS, MARGO R.
; APPLICANT: DULL, THOMAS J.
; APPLICANT: ZSEBO, KRISTINA M.
; APPLICANT: QIN, LU
; TITLE OF INVENTION: METHOD FOR PRODUCTION OF HIGH TITER
; TITLE OF INVENTION: VIRUS AND HIGH EFFICIENCY RETROVIRAL MED
; TITLE OF INVENTION: OF MAMMALIAN CELLS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CELL GENESYS, INC.
; STREET: 322 LAKESIDE DRIVE
; CITY: FOSTER CITY
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,582
; FILING DATE: 10-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/258,152
; FILING DATE: 10-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/076,299
; FILING DATE: 11-JUN-93
; ATTORNEY/AGENT INFORMATION:
; NAME: KRUPEN, KAREN I.
; REGISTRATION NUMBER: 34,647
; REFERENCE/DOCKET NUMBER: CELL 13.2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-358-9600 X131
; TELEFAX: 415-349-7392
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:

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26 base pairs
nucleic acid
NESS: single
: linear
YPE: DNA (genomic)
4

51.4%; Score 14.4; DB 2; Length 26;
milarity 75.0%; Pred. No. 2e+03; 6; Indels 0; Gaps 0;
Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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CACCTTCTTCAAGTGCAGATCTT 2

4/c
Application US/09266596
18187

RMATION:
FINER, MITCHELL H.
DULL, THOMAS J.
ZSEBO, KRISZTINA M.
COOKE, KEEGAN
FARSON, DEBORAH A.

INVENTION: METHOD FOR PRODUCTION OF HIGH TITER
NVENTION: VIRUS AND HIGH EFFICIENCY RETROVIRAL MEDIATED TRANSDUCTION
NVENTION: OF MAMMALIAN CELLS
SEQUENCES: 48

ENCE ADDRESS:
E: CELL GENESYS, INC.
322 LAKESIDE DRIVE
OSTER CITY
CALIFORNIA
USA

404

READABLE FORM:
YPE: Floppy disk

: IBM PC compatible
3 SYSTEM: PC-DOS/MS-DOS

: Patent In Release #1.0, Version #1.25

PLICATION DATA:

ION NUMBER: US/09/266,596

ATE:

CATION:

ICATION DATA:

ION NUMBER: 08/517,488

ATE: 21-AUG-1995

ION NUMBER: US 08/258,152

ATE: 10-JUN-1994

ICATION DATA:

ION NUMBER: US 08/076,299

ATE: 11-JUN-1993

SENT INFORMATION:

RUPEN, KAREN I.

TION NUMBER: 34,647

E/DOCKET NUMBER: CELL 13.3

ICATION INFORMATION:

E: 415-358-9600 X131

415-349-7392

FOR SEQ ID NO: 14:

CHARACTERISTICS:

26 base pairs

nucleic acid

NESS: single

: linear

YPE: DNA (genomic)

4

51.4%; Score 14.4; DB 3; Length 26;
milarity 75.0%; Pred. No. 2e+03; 6; Indels 0; Gaps 0;
Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5 TCATCTCTGTCAGTGCAGTGCAT 28
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Db 25 TCACCTTCTTCAAGTGCAGATCTT 2

RESULT 11

US-08-479-737-8/c
; Sequence 8, Application US/08479737
; Patent No. 6319494

; GENERAL INFORMATION:

; APPLICANT: Capon, Daniel J
; Weiss, Arthur A
; Irving, Brian A
; Roberts, Margo R
; Zsebo, Krisztina

; TITLE OF INVENTION: CHIMERIC CHAINS FOR RECEPTOR ASSOCIATE
; SIGNAL TRANSDUCTION PATHWAYS

; NUMBER OF SEQUENCES: 51

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CELL GENESYS, INC.

; STREET: 322 Lakeside Drive

; CITY: Foster City

; STATE: California

; COUNTRY: USA

; ZIP: 94404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/479,737

; FILING DATE: 07-Jun-1995

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/238,405

; FILING DATE: 05-MAY-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Mandel, Saralynn

; REGISTRATION NUMBER: 31,853

; REFERENCE/DOCKET NUMBER: Cell 5.3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 358-9600

; TELEFAX: (415) 358-0803

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 26 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-08-479-737-8

Query Match

51.4%; Score 14.4; DB 4; Length 26;

Best Local Similarity 75.0%; Pred. No. 2e+03;

Matches 18; Conservative 0; Mismatches 6; Indels 0;

QY 5 TCATCTCTGTCAGTGCAGTGCAT 28
|||||
Db 25 TCACCTTCTTCAAGTGCAGATCTT 2

RESULT 12

US-08-475-442A-8/c

; Sequence 8, Application US/08475442A

; Patent No. 6407221

; GENERAL INFORMATION:

; APPLICANT: CAPON, DANIEL J

; APPLICANT: WEISS, ARTHUR

; APPLICANT: IRVING, BRIAN A

; APPLICANT: ROBERTS, MARGO R

ZSEBO, KRISZTINA
INVENTION: CHIMERIC CHAINS FOR
RECEPTOR-ASSOCIATED SIGNAL TRANSDUCTION PATHWAYS
SEQUENCES: 51
PENCE ADDRESS:
ZSEBO, KRISZTINA
322 LAKESIDE DRIVE
FOSTER CITY
CALIFORNIA
USA
1404
READABLE FORM:
TYPE: Floppy disk
t: IBM PC compatible
g SYSTEM: PC-DOS/MS-DOS
3: PatentIn Release #1.0, Version #1.25
PLICATION DATA:
TION NUMBER: US/08/475,442A
DATE: 06-JUN-1995

ICATION DATA:
TION NUMBER: US 08/238,405
DATE: 05-MAY-1994
ICATION DATA:
TION NUMBER: US 07/988,194
DATE: 09-DEC-1992
ICATION DATA:
TION NUMBER: US 07/627,643
DATE: 14-DEC-1990
ICATION DATA:
TION NUMBER: PCT/US91/09431
DATE: 12-DEC-1991
AGENT INFORMATION:
KRUPEN, KAREN I
TION NUMBER: 34,647
E/DOCKET NUMBER: CELLS.5
ICATION INFORMATION:
NR: (415)358-9600X131
FOR SEQ ID NO: 8:
CHARACTERISTICS:
26 base pairs
nucleic acid
NESS: single
t: linear
TYPE: cDNA
-8

51.4%; Score 14.4; DB 4; Length 26;
Similarity 75.0%; Pred.No.2e+03; 6; Indels 0; Gaps 0;
Conservative 0; Mismatches 6;

TCATCCTCTGCATGTCAGGTGTCAT 28
TCACCTTCTTCAAGTCAGATCTT 2

14/c
Application US/09944411
306604
FORMATION:
CANT: FINER, MITCHELL H.
DULL, THOMAS J.
ZSEBO, KRISZTINA M.
COOKE, KEEGAN
FARSON, DEBORAH A.
OF INVENTION: METHOD FOR PRODUCTION OF HIGH TITER
VIRUS AND HIGH EFFICIENCY RETROVIRAL MEDIATED TRANSDUCTION
OF MAMMALIAN CELLS

R OF SEQUENCES: 48
SPONSOR ADDRESS:
ADDRESSEE: CELL GENESYS, INC.

STREET: 322 LAKESIDE DRIVE
CITY: FOSTER CITY
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/944,411
FILING DATE: 04-Sep-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/914,893
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/258,152
FILING DATE: 10-JUN-1994
APPLICATION NUMBER: US 08/076,299
FILING DATE: 11-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: KRUPEN, KAREN I.
REGISTRATION NUMBER: 34,647
REFERENCE/DOCKET NUMBER: CELL 13.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-358-9600 X131
TELEFAX: 415-349-7392
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-944-411-14

Query Match 51.4%; Score 14.4; DB 4; Length 26;
Best Local Similarity 75.0%; Pred.No.2e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0.

Qy 5 TCATCCTCTGCATGTCAGGTGTCAT 28
Db 25 TCACCTTCTTCAAGTCAGATCTT 2

RESULT 14

US-08-439-813-1
Sequence 1, Application US/08439813
Patent No. 5631133
GENERAL INFORMATION:
APPLICANT: HANAHAN, Douglas
APPLICANT: YAMAMOTO, Keith
APPLICANT: VIVENCO, Maria del Mar
TITLE OF INVENTION: A TRANSITION IN TRANSCRIPTIONAL ACTIVATI
TITLE OF INVENTION: INTRACELLULAR HORMONE RECEPTORS AT THE T
TITLE OF INVENTION: DEVELOPMENT
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Street Tower, 20th
STREET: Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

ION NUMBER: US/08/439,813
DATE: 12-MAY-1995
CATION: 435
GENT INFORMATION:
harrett-Wackowski, Eugenia
TION NUMBER: 37,330
E/DOCKET NUMBER: 02307E-059800
ICATION INFORMATION:
IE: 415/543-9600
415/543-5043
FOR SEQ ID NO: 1:
HARACTERISTICS:
42 base pairs
nucleic acid
NESS: single
: linear
YPE: DNA (genomic)

51.4%; Score 14.4; DB 1; Length 42;
milarity 75.0%; Pred. No. 2.2e+03;
Conservative 0; Mismatches 6; Indels 0; Gaps 0;

GCATCATCTCTGTCATGTCAGG 24
|||||
ACATCAITCTGCGTCGCCAGG 41

-1
Application PC/TUS9605291A

THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
NVENTION: A TRANSITION IN TRANSCRIPTIONAL ACTIVATION BY
NVENTION: INTRACELLULAR HORMONE RECEPTORS AT THE TUMOR STAGE
NVENTION: OF DERMAL FIBROSARCOMA DEVELOPMENT
SEQUENCES: 3

ENCE ADDRESS:
E: Robbins, Berliner & Carson
201 N. Figueroa Street, 5th Floor
os Angeles
California
USA

012-2628
EADABLE FORM:
YPE: Floppy disk
: IBM PC compatible
G SYSTEM: PC-DOS/MS-DOS
: Patentin Release #1.0, Version #1.30
PLICATION DATA:
ION NUMBER: PCT/US96/05291A

DATE:
CATION:
GENT INFORMATION:
erliner, Robert
TION NUMBER: 20,121
E/DOCKET NUMBER: 5555-382
ICATION INFORMATION:
IE: 213-977-1001
213-977-1003
FOR SEQ ID NO: 1:
HARACTERISTICS:
42 base pairs
nucleic acid
NESS: single
: linear
YPE: DNA (genomic)

-1
51.4%; Score 14.4; DB 5; Length 42;
milarity 75.0%; Pred. No. 2.2e+03;
Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AGCATCATCTCTGTCATGTCAGG 24
|
Db 18 AACATCATGTTCTGCGTCGCCAGG 41

RESULT 16
US-09-383-143-20
; Sequence 20, Application US/09383143
; Patent No. 6372429
; GENERAL INFORMATION:
; APPLICANT: SHARON, GIL
; TITLE OF INVENTION: METHOD FOR ASSEMBLY OF MULTIPLE DNA FRAGMENT
; FILE REFERENCE: LUZZATTO 3.3-061 CONT
; CURRENT APPLICATION NUMBER: US/09/383,143
; CURRENT FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: PCT/IL98/00096
; PRIOR FILING DATE: 1998-02-26
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Combined DNA/RNA Molecule: P
US-09-383-143-20

Query Match 51.4%; Score 14.4; DB 4; Length 47;
Best Local Similarity 54.2%; Pred. No. 2.2e+03;
Matches 13; Conservative 5; Mismatches 6; Indels 0;

Qy 1 AGCATCATCTCTGTCATGTCAGG 24
|
Db 2 AUCAUCAUCAUCAUCAUCAUG 25

RESULT 17
US-09-158-863C-43/c
; Sequence 43, Application US/09158863C
; Patent No. 6280978
; GENERAL INFORMATION:
; APPLICANT: Mitchell, Lloyd G.
; APPLICANT: Garcia-Blanco, Mariano A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USE IN
; FILE REFERENCE: 31304-B-A
; CURRENT APPLICATION NUMBER: US/09/158,863C
; CURRENT FILING DATE: 1998-09-23
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 09/133,717
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 08/766,354
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: 60/008,317
; PRIOR FILING DATE: 1995-12-07
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 43
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-158-863C-43

Query Match 51.4%; Score 14.4; DB 3; Length 51;
Best Local Similarity 75.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0;

Qy 1 AGCATCATCTCTGTCATGTCAGG 24
|
Db 35 AGCATCATCATCATCATCATG 12

```

10 Application US/08687865A
   55596
RMATION:
   Jones, Kevin F.
   Zagursky, Robert J.
   Ooi, Peggy
INVENTION: The NuCA Protein of Haemophilus
INVENTION: influenzae and the Gene Encoding That Protein
SEQUENCES: 23
ENCE ADDRESS:
   American Cyanamid Company
   One Cyanamid Plaza
   Wayne
   New Jersey
   U.S.A.
7470
READABLE FORM:
TYPE: Floppy disk
t: IBM PC compatible
G SYSTEM: PC-DOS/MS-DOS
: PatentIn Release #1.0, Version #1.30
PLICATION DATA:
ION NUMBER: US/08/687,865A
DATE: 26-JUL-1996
CATION: 536
AGENT INFORMATION:
   Jordan, Alan M.
ATION NUMBER: 30,637
E/DOCKET NUMBER: 33,250-00
ICATION INFORMATION:
   201-831-3244
   201-831-3305
FOR SEQ ID NO: 10:
53 base pairs
nucleic acid
NESS: single
f: linear
TYPE: DNA (genomic)
-10
51.4%; Score 14.4; DB 2; Length 53;
milarity 75.0%; Pred. No. 2.2e+03;
: Conservative 0; Mismatches 6; Indels 0; Gaps 0;
AGCATCATCTCTGTCATGTCAGG 24
ATCATCATCATCATCATGTCATGG 53

10 Application US/09043711
221365
RMATION:
   Jones, Kevin F.
   Zagursky, Robert J.
   Ooi, Peggy
INVENTION: The NuCA Protein of Haemophilus
INVENTION: influenzae and the Gene Encoding That Protein
SEQUENCES: 23
ENCE ADDRESS:
   American Cyanamid Company
   One Cyanamid Plaza
   Wayne
   New Jersey
   U.S.A.
7470
READABLE FORM:
TYPE: Floppy disk
R: IBM PC compatible

```

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/043,711
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/687,865
; FILING DATE: 26-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gordon, Alan M.
; REGISTRATION NUMBER: 30,637
; REFERENCE/DOCKET NUMBER: 33,250-00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3244
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-043-711-10

Query Match 51.4%; Score 14.4; DB 3; Length 53;
Best Local Similarity 75.0%; Pred. No. 2.2e+03;
Matches 18; Conservative 0; Mismatches 6; Indels 0,

Qy 1 AGCATCATCTCTGTCATGTCAGG 24
Db 30 ATCATCATCATCATCATGTCATGG 53

RESULT 20
US-08-687-865A-11/c
; Sequence 11, Application US/08687865A
; Patent No. 5955596
; GENERAL INFORMATION:
; APPLICANT: Jones, Kevin F.
; APPLICANT: Zagursky, Robert J.
; APPLICANT: Ooi, Peggy
; TITLE OF INVENTION: The NuCA Protein of Haemophilus
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07470
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,865A
; FILING DATE: 26-JUL-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Gordon, Alan M.
; REGISTRATION NUMBER: 30,637
; REFERENCE/DOCKET NUMBER: 33,250-00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3244
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 55 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

```

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us-10-090-326-23.max.rni

```
: linear
YPE: DNA (genomic)
11
    51.4%; Score 14.4; DB 2; Length 55;
milarity 75.0%; Pred.No. 2.3e+03;
Conservative 0; Mismatches 6; Indels 0; Gaps 0;

GCATCATCCTCTGCATGGTCAGG 24
||||| ||| ||||| ||
TCATCATCATCATCATGGTATGG 5

1/c
Application US/09043711
21365
RMATION: Kevin F.
        Zagursky, Robert J.
        Ooi, Peggy
NVENTION: The NuCA Protein of Haemophilus
NVENTION: Influenzae and the Gene Encoding That Protein
SEQUENCES: 23
ENCE ADDRESS:
E: American Cyanamid Company
    One Cyanamid Plaza
    ayne
    New Jersey
    U.S.A.
470
EADABLE FORM:
YPE: Floppy disk
E: IBM PC compatible
G SYSTEM: PC-DOS/MS-DOS
    : PatentIn Release #1.0, Version #1.30
PLICATION DATA:
ION NUMBER: US/09/043,711
ATE:
CATION:
ICATION DATA:
ION NUMBER: US 08/687,865
ATE: 26-JUL-1996
GENT INFORMATION:
    ordon, Alan M.
TION NUMBER: 30,637
E/DOCKET NUMBER: 33,250-00
ICATION INFORMATION:
E: 201-831-3244
    201-831-3305
FOR SEQ ID NO: 11:
HARACTERISTICS:
    55 base pairs
    ucleic acid
    NESS: single
: linear
YPE: DNA (genomic)
1
    51.4%; Score 14.4; DB 3; Length 55;
milarity 75.0%; Pred.No. 2.3e+03;
Conservative 0; Mismatches 6; Indels 0; Gaps 0;

GCATCATCCTCTGCATGGTCAGG 24
||||| ||| ||||| ||
TCATCATCATCATCATGGTATGG 5

3
Application US/09490692
80353
MATION:
: APPLICANT: Nicholas M. Dean
: APPLICANT: Lex M. Cowser
: TITLE OF INVENTION: ANTISENSE MODULATION OF DAXX EXPRESSION
: FILE REFERENCE: RTS-0120
: CURRENT APPLICATION NUMBER: US/09/490,692
: CURRENT FILING DATE: 2000-01-24
: NUMBER OF SEQ ID NOS: 176
: SEQ ID NO 13
: LENGTH: 29
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: PCR Probe
: US-09-490-692-13

Query Match 50.7%; Score 14.2; DB 3; Length 29;
Best Local Similarity 84.2%; Pred.No. 2.5e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0;

Qy 2 GCATCATCCTCTGCATGGT 20
Db 7 GCAACATCCTCTCCAGGT 25

RESULT 23
US-09-144-428-61/c
: Sequence 61, Application US/09144428
: Patent No. 6583108
: GENERAL INFORMATION:
: APPLICANT: BAYER CORPORATION, The
: APPLICANT: TAMBURINI, Paul P
: APPLICANT: DAVIS, Gary
: APPLICANT: DELARIA, Katherine A
: APPLICANT: MARLOR, Christopher W
: APPLICANT: MULLER, Daniel K
: TITLE OF INVENTION: HUMAN BIKUNIN
: NUMBER OF SEQUENCES: 71
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
: STREET: 300 S. Wacker Drive Suite 3200
: CITY: CHICAGO
: STATE: ILLINOIS
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/144,428
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: WO PCT/US97/03894
: FILING DATE: 10-MAR-1997
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/013,106
: FILING DATE: 11-MAR-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/019,793
: FILING DATE: 14-JUN-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/725,251
: FILING DATE: 04-OCT-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: CHAO, Mark
: REGISTRATION NUMBER: 37,293
: REFERENCE/DOCKET NUMBER: 96,223-II
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (312) 913-0001
: TELEFAX: (312) 913-0002
```

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us-10-090-326-23.max.rni

FOR SEQ ID NO: 61:
CHARACTERISTICS:
45 base pairs
nucleic acid
NESS: unknown
: not relevant
TYPE: DNA (genomic)
1

50.7%; Score 14.2; DB 4; Length 45;
Similarity 84.2%; Pred. No. 2.7e+03;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CTCTGATGTCAGTCA 27
|||||
ATCTGAGGCCAGTCA 12

0 Application US/08652558
61155

INVENTION:
LIN, AUGUSTINE YEE-THARN
INVENTION: HUMANIZED ANTIBODIES AND USES
SEQUENCES: 52
ENCE ADDRESS:
E: BANNER & WITCOFF
75 STATE STREET, 23RD FLOOR
OSTON
MASSACHUSETTS
USA

109
EADABLE FORM:
YPE: 3.5 inch diskette, 1.4 Mb storage
G SYSTEM: PC-DOS/MS-DOS
: WordPerfect 6.1
PLICATION DATA:
ION NUMBER: US/08/652,558
ATE: JUNE 6, 1996

ICATION DATA:
ION NUMBER: PCT/IB94/00387
ATE: NOVEMBER 21, 1994
GENT INFORMATION:
ANKWICH, LEON R.
TION NUMBER: 30,237
E/DOCKET NUMBER: 95,497-L
ICATION INFORMATION:
E: 617-345-9100
617-345-9111

FOR SEQ ID NO: 30:
HARACTERISTICS:
51 base pairs
nucleic acid
NESS: single
: linear
TYPE: cDNA
10

50.7%; Score 14.2; DB 2; Length 51;
Similarity 84.2%; Pred. No. 2.7e+03;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TCATCATCTCTGATGCT 20
|||||
TATCATCTCTCTTGT 49

Application US/08483636

; Patent No. 591411C
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSER: SmithKline Beecham Corp./Corporate
; ADDRESSER: Intellectual Property
; STREET: P.O. Box 1539 / UW2220
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,636
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/117366
; FILING DATE: 07-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/136783
; FILING DATE: 14-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US/94/10308
; FILING DATE: 07-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Sutton, Jeffrey A.
; REGISTRATION NUMBER: 34,028
; REFERENCE/DOCKET NUMBER: P50186-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 270-5024
; TELEFAX: (215) 270-5090
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 57 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..57
; US-08-483-636-7

Query Match 50.7%; Score 14.2; DB 2; Length 57;
Best Local Similarity 84.2%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0;

Qy 2 GCATCATCTCTGATGCT 20
| | | | | | | | | | | | | | | | | | | | | |
Db 14 GTATCATCTCTCTTGT 32

RESULT 26
US-08-483-632-7
; Sequence 7, Application US/08483632
; Patent No. 5928904
; GENERAL INFORMATION:
; APPLICANT: Holmes, Stephen D.
; APPLICANT: Gross, Mitchell S.
; APPLICANT: Sylvester, Daniel R.
; TITLE OF INVENTION: Recombinant IL4 Antibodies Useful in
; TITLE OF INVENTION: Treatment of IL4 Mediated Disorders
; NUMBER OF SEQUENCES: 75

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us-10-090-326-23.max.rni

NCE ADDRESS:
: SmithKline Beecham Corp./Corporate
: Intellectual Property
P.O. Box 1539 / UW2220
ing of Prussia
A
USA
06-0939
ADABLE FORM:
PE: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patent In Release #1.0, Version #1.25
LICATON DATA:
ON NUMBER: US/08/483,632
TE:
ATION:
CATION DATA:
ON NUMBER: US 08/117366
TE: 07-SEP-1993
CATION DATA:
ON NUMBER: US 08/136783
TE: 14-OCT-1993
CATION DATA:
ON NUMBER: PCT/US/94/10308
TE: 07-SEP-1994
ENT INFORMATION:
enton, Jeffrey A.
ION NUMBER: 34,028
ION NUMBER: P50186-3
CATION INFORMATION:
: (215) 270-5024
OR SEQ ID NO: 7:
CHARACTERISTICS:
57 base pairs
iclic acid
ESS: double
unknown
PE: CDNA
CDS
1..57
50.7%; Score 14.2; DB 2; Length 57;
ilarity 84.2%; Pred. No. 2.8e+03;
Conservative 0; Mismatches 3; Indels 0; Gaps 0;
ATCATCCTCTGCGATGGT 20
ATCATCCTCTCTTGTGT 32
5/c
pplication US/08454899G
2503
ATION:
abb, Roy R.
arr, Frank J.
tempest, Philip R.
ENTION: RECOMBINANT ANTI-VLA4 ANTIBODY MOLECULES
E: 10274-007001
ICATION NUMBER: US/08/454,899G
NG DATE: 1995-05-31
ATION NUMBER: US 08/004,798
DATE: 1993-01-12
ATION NUMBER: PCT/US94/00266
DATE: 1994-01-07
ID NOS: 109
stSEQ for Windows Version 4.0

; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide for vector construction
US-08-454-899G-95
Query Match 50.7%; Score 14.2; DB 4; Length 57;
Best Local Similarity 84.2%; Pred. No. 2.8e+03;
Matches 16; Conservative 0; Mismatches 3; Indels 0;
QY 2 GCATCATCCTCTGCGATGGT 20
Db 40 GCATCATCCTCTTGTGT 22
RESULT 28
US-09-158-863C-35/c
; Sequence 35, Application US/09158863C
; Patent No. 6280978
; GENERAL INFORMATION:
; APPLICANT: Mitchell, Lloyd G.
; APPLICANT: Garcia-Blanco, Mariano A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USE IN
; TITLE OF INVENTION: SPLICEOSOME MEDIATED RNA TRANS-SPLICING
; FILE REFERENCE: 31304-B-A
; CURRENT APPLICATION NUMBER: US/09/158,863C
; CURRENT FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 09/133,717
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 09/087,233
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 08/766,354
; PRIOR FILING DATE: 1996-12-13
; PRIOR APPLICATION NUMBER: 60/008,317
; PRIOR FILING DATE: 1995-12-07
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 35
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primers complementary to beta
; OTHER INFORMATION: gene (accession #X00266)
US-09-158-863C-35
Query Match 50.0%; Score 14; DB 3; Length 35;
Best Local Similarity 77.3%; Pred. No. 3.1e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0;
QY 1 AGCATCATCCTCTGCGATGGTCA 22
Db 28 AGCAGCAGCCCTCGCAGGGTTA 7
RESULT 29
US-08-428-370A-1/c
; Sequence 1, Application US/08428370A
; Patent No. 5569583
; GENERAL INFORMATION:
; APPLICANT: Greenberg, Steven J.
; APPLICANT: Evans, Mary Jo
; TITLE OF INVENTION: Rapid and Sensitive Detection of
; TITLE OF INVENTION: Herpesviruses
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hodgson, Russ, Andrews, Woods & Goodyear
; STREET: 1800 One M&T Plaza
; CITY: Buffalo
; STATE: New York
; COUNTRY: United States
; ZIP: 14203-2391

us-10-090-326-23.max.rni

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; TELEFAX: 716-849-0349
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single-stranded
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Cytomegalovirus
; FEATURE:
; LOCATION: GenBank locus H55MIEG
US-08-600-764-1

Query Match 50.0%; Score 14; DB 2; Length 38;
Best Local Similarity 77.3%; Pred No. 3.2e+03;
Matches 17; Conservative 0; Mismatches 5; Indels 0;

QY 6 CATCCTCTGCATGGTCAGGTCA 27
    ||| ||| ||| ||| ||| ||| |||
Db 33 CATGCTCTGCATAGTTAGCCCA 12

RESULT 31
US-09-517-467B-294
; Sequence 294, Application US/09517467B
; Patent No. 6451602
; GENERAL INFORMATION:
; APPLICANT: Ian Popoff
; APPLICANT: Lex M. Cowsett
; TITLE OF INVENTION: ANTISENSE MODULATION OF PARP EXPRESSION
; FILE REFERENCE: RTS-0150
; CURRENT APPLICATION NUMBER: US/09/517,467B
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 09/517,467
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 345
; SEQ ID NO 294
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-517-467B-294

Query Match 49.3%; Score 13.8; DB 4; Length 20;
Best Local Similarity 88.2%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0;

QY 2 GCATCATCTCTGCATG 18
    ||| ||| ||| ||| ||| |||
Db 2 GCCTCATCTCTGCCTG 18

RESULT 32
US-08-777-405A-7/c
; Sequence 7, Application US/08777405A
; Patent No. 5858753
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: No. 5858753el Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall O'Toole Garstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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3 09:04:21 2004

us-10-090-326-23.max.rni

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; SYSTEM: PC-DOS/MS-DOS
; PatentIn Release #1.0, Version #1.30
PLICATION DATA:
ION NUMBER: US/08/777,405A
ATE:
TATION: 435
ENT INFORMATION:
. 5858753and, Greta E.
ION NUMBER: 35,302
E/DOCKET NUMBER: 27866/33441
ICATION INFORMATION:
2: (312) 474-6300
25-3856
FOR SEQ ID NO: 7:
CHARACTERISTICS:
21 base pairs
ucleic acid
NESS: single
YPE: other nucleic acid
7
49.3%; Score 13.8; DB 2; Length 21;
nilarity 88.2%; Pred. No. 3.5e+03; Indels 0; Gaps 0;
Conservative 0; Mismatches 2;
PCCTCTGCATGCTCAG 23
|||||
TCATCTGCAGGGTCTCAG 5

7/c
plication US/08977871A
82910
RMATION:
Chantry, David
Hoekstra, Merl F.
Holtzman, Douglas A
NVENTION: No. 5882910el Lipid Kinase
SEQUENCES: 17
ENCE ADDRESS:
3: Marshall O'Toole Gerstein Murray & Borun
6300 Sears Tower/233 South Wacker Drive
chicago
Illinois
USA
506
SADABLE FORM:
YPE: Floppy disk
: IBM PC compatible
3 SYSTEM: PC-DOS/MS-DOS
PLICATION DATA:
ION NUMBER: US/08/977,871A
ATE:
CATION:
ICATION DATA:
ION NUMBER: 08/777,405
ATE:
GENT INFORMATION:
o. 5882910and, Greta E.
TION NUMBER: 35,302
E/DOCKET NUMBER: 27866/33441
ICATION INFORMATION:
E: (312) 474-6300
25-3856
FOR SEQ ID NO: 7:
CHARACTERISTICS:
21 base pairs
ucleic acid
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-977-871A-7
Query Match 49.3%; Score 13.8; DB 2; Length 21;
Best Local Similarity 88.2%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0;
QY 7 ATCCTCTGCATGCTCAG 23
||| |||||
Db 21 ATCATCTGCAGGGTCTCAG 5

RESULT 34
US-09-225-951-7/c
; Sequence 7, Application US/09225951
; Patent No. 5985589
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Hoekstra, Merl F.
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: No. 5985589el Lipid Kinase
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall O'Toole Gerstein Murray & Borun
; STREET: 6300 Sears Tower/233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/225,951
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5985589and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/33441
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-09-225-951-7
Query Match 49.3%; Score 13.8; DB 2; Length 21;
Best Local Similarity 88.2%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0;
QY 7 ATCCTCTGCATGCTCAG 23
||| |||||
Db 21 ATCATCTGCAGGGTCTCAG 5

RESULT 35
US-09-253-396A-67/c
; Sequence 67, Application US/09253396A
; Patent No. 6205404
; GENERAL INFORMATION:
; APPLICANT: Genome Dynamics, Inc.
; TITLE OF INVENTION: DNA-Binding Proteins of the Zinc-Finger Cla
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FILE: 1116242-0003 file: genome03F.app
SEQ NUMBER: US/09/253,396A
SEQ DATE: 1999-02-19
SEQ ID NOS: 231
acntin ver. 2.0

accharomyces cerevisiae

67

49.3%; Score 13.8; DB 3; Length 27;
ilarity 86.2%; Pred. No. 3.7e+03;
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

TCATCCTCTGCGATGGT 20
|||||
TCATCCTGGGCGATGGT 11

31 Application US/08646789A

22863

RMATION:

Peyman, John A.

INVENTION: REGULATION OF GENE EXPRESSION

SEQUENCES: 101

ENCE ADDRESS:

E: PENNIE & EDMONDS

1155 Avenue of the Americas

ew York

New York

U.S.A.

036-2711

ADABLE FORM:

YPE: Floppy disk

: IBM PC compatible

IG SYSTEM: PC-DOS/MS-DOS

: Patent in Release #1.0, Version #1.30

PLICATION DATA:

ION NUMBER: US/08/646,789A

DATE: May 21, 1996

ICATION: 800

AGENT INFORMATION:

isrock, S. Leslie

ATION NUMBER: 18,872

BE/DOCKET NUMBER: 6523-006

ICATION INFORMATION:

BE: (212) 790-9090

(212) 869-9741/8864

66141 PENNIE

FOR SEQ ID NO: 31:

CHARACTERISTICS:

29 base pairs

nucleic acid

NESS: single

f: linear

TYPE: DNA

-31

49.3%; Score 13.8; DB 3; Length 29;
ilarity 72.0%; Pred. No. 3.7e+03;
Conservative 0; Mismatches 7; Indels 0; Gaps 0;

ATCATCCTCTGCGATGGTTCAGT 28

|||||

ATGTTGCTCTGTATGTAAGACAT 27

-23

Application US/09354231B

Patent No. 6342658
GENERAL INFORMATION:
APPLICANT: DeBonte, Lorin R.
APPLICANT: Shorosh, Basil S.
TITLE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES
FILE REFERENCE: 07148-063002
CURRENT APPLICATION NUMBER: US/09/354,231B
CURRENT FILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: US 08/874,109
PRIOR FILING DATE: 1997-06-12
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 32
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: primer
US-09-354-231B-23

Query Match 49.3%; Score 13.8; DB 4; Length 32;
Best Local Similarity 60.0%; Pred. No. 3.7e+03;
Matches 15; Conservative 3; Mismatches 7; Indels 0;

Qy 1 AGCATCATCTCTGCGATGGTTCAGGT 25

Db 2 AUCAUCAUCAUCITCTTCGTAGGGT 26

RESULT 38

US-09-128-602B-23

Sequence 23, Application US/09128602B

Patent No. 6414223

GENERAL INFORMATION:

APPLICANT: Kodali, Dharna

APPLICANT: Fan, Zhegong

APPLICANT: DeBonte, Lorin R.

TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TC

FILE REFERENCE: 07148-072001

CURRENT APPLICATION NUMBER: US/09/128,602B

CURRENT FILING DATE: 1998-08-03

NUMBER OF SEQ ID NOS: 68

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 23

LENGTH: 32

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: primer

US-09-128-602B-23

Query Match 49.3%; Score 13.8; DB 4; Length 32;
Best Local Similarity 60.0%; Pred. No. 3.7e+03;
Matches 15; Conservative 3; Mismatches 7; Indels 0;

Qy 1 AGCATCATCTCTGCGATGGTTCAGGT 25

Db 2 AUCAUCAUCAUCITCTTCGTAGGGT 26

RESULT 39

US-09-995-297-23

Sequence 23, Application US/09995297

Patent No. 6649782

GENERAL INFORMATION:

APPLICANT: Kodali, Dharna

APPLICANT: Fan, Zhegong

APPLICANT: DeBonte, Lorin R.

TITLE OF INVENTION: PLANTS, SEEDS AND OILS HAVING AN ELEVATED TC

FILE REFERENCE: 07148-072002

CURRENT APPLICATION NUMBER: US/09/995,297

09:04:21 2004

us-10-090-326-23.max.rni

NG DATE: 2001-11-27
ATION NUMBER: US 09/128.602
DATE: 1998-08-03
ID NOS: 68
stSEQ for Windows Version 4.0

rtificial Sequence

ATION: primer

49.3%; Score 13.8; DB 4; Length 32;
ilarity 60.0%; Pred. No. 3.7e+03;
Conservative 3; Mismatches 7; Indels 0; Gaps 0;

3CATCATCTCTGTCAGGT 25

JCAUCAUCAUCTTCTCGTAGGT 26

plication US/08439585

07831

RMATION:

Apler, Heiner; Beinink, Jergen;

Dorschug, Michael; Gottschalk, Uwe

VENTION: PROCESS FOR PREPARING

VENTION: RECOMBINANT APROTININ AND RECOMBINANT

VENTION: APROTININ VARIANTS HAVING THE NATURAL N-

VENTION: TERMINAL SEQUENCE

SEQUENCES: 4

ENCE ADDRESS:

S. SPRUNG HORN KRAMER & WOODS

660 White Plains Road

arrytown

New York

U.S.A.

591-5144

ADABLE FORM:

YPE: Diskette, 3.50 inch, 1.44MB

YPE: storage

: NEC Powermate SX/20

G SYSTEM: DOS

: WordPerfect 5.1

PLICATION DATA:

ION NUMBER: US/08/439,585

ATE: 11-MAY-1995

CATION: 435

ICATION DATA:

ION NUMBER: P 44 17 353.9 (Germany)

ATE: 18-MAY-1994

GENT INFORMATION:

urt G. Briscoe

TION NUMBER: 33,141

E/DOCKET NUMBER: Bayer 9285-KGB

ICATION INFORMATION:

E: (914) 332-1700

(914) 332-1844

FOR SEQ ID NO: 1:

HARACTERISTICS:

42 base pairs

nucleic acid

NESS: single

: linear

YPE: DNA (genomic)

AL: no

: no

Query Match 49.3%; Score 13.8; DB 1; Length 42;
Best Local Similarity 72.0%; Pred. No. 3.9e+03;
Matches 18; Conservative 0; Mismatches 7; Indels 0;

QY 2 GCATCATCTCTGTCAGGTTCAGGTTC 26

Db 1 GCAGCATCTCTCGCATTAGCTCGTC 25

Search completed: April 12, 2004, 19:17:31

Job time : 113.179 secs

09:04:21 2004

us-10-090-326-23.max.rng

GenCore version 5.1.6
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leic search, using sw model

April 12, 2004, 14:34:57 ; Search time 109.077 Seconds
(without alignments)
1090.511 Million cell updates/sec

US-10-090-326-23

28 1 agcatcatcctcgcagtgcat 28

IDENTITY NUC

Gapop 10.0 ; Gapext 1.0

3373863 seqs, 2124099041 residues

hits satisfying chosen parameters: 3308108

length: 0
length: 60

Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

N_Geneseq_29Jan04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2003as:*
- 8: Geneseqn2003bs:*
- 9: Geneseqn2003cs:*
- 10: Geneseqn2004s:*

is the number of results predicted by chance to have a
ter than or equal to the score of the result being printed,
ived by analysis of the total score distribution.

SUMMARIES

Query	Match	Length	DB	ID	Description
100.0	28	6	ABQ82557	Internal	Abq82557 Internal
71.4	20	2	AAV84287	LacZ repo	AAV84287 LacZ repo
71.4	20	6	ABT08197	Recombina	Abt08197 Recombina
71.4	20	9	ADB81355	PCR prime	ADB81355 PCR prime
67.9	19	2	AAV82445	LacZ gene	AAV82445 LacZ gene
64.3	30	2	AAV82380	H. vulgar	AAV82380 H. vulgar
62.1	30	6	ABN50202	Human spl	Abn50202 Human spl
61.4	40	6	ABT12156	E coli ex	Abt12156 E coli ex
60.7	40	6	ABT12155	E coli ex	Abt12155 E coli ex
60.0	60	6	ABN48389	Human spl	Abn48389 Human spl
57.1	29	2	AAQ51481	Dengue vi	AAQ51481 Dengue vi
57.1	42	2	AAV39800	Oligonucl	AAV39800 Oligonucl
55.7	30	2	AAV45436	Aspergill	AAV45436 Aspergill
55.0	60	6	ABN39943	Human spl	Abn39943 Human spl
55.0	60	6	ABN37161	Human spl	Abn37161 Human spl
54.3	33	3	AA68232	Angiogene	AA68232 Angiogene
54.3	39	5	AAV75700	Human GAD	AAV75700 Human GAD
54.3	56	2	AAV20388	Primer 5	AAV20388 Primer 5
54.3	58	6	AAI72186	Primer CD	AAI72186 Primer CD
54.3	60	6	ABN47436	Human spl	Abn47436 Human spl
53.6	25	8	ACT09245	Human mic	Act09245 Human mic
53.6	41	6	AAH88866	Aldehyde/	AAH88866 Aldehyde/
53.6	44	4	AAH43442	Primer J	AAH43442 Primer J

50.0	29	2	AAV44876	Aav44876 Probe for	c 170	13.8	49.3	52	6	AA138810	Aa138810
50.0	29	5	AAF98550	Aaf98550 Human cDN	c 171	13.8	49.3	52	6	ABK46276	Abk46276
50.0	30	2	Az09724	S. cerevi	c 172	13.8	49.3	52	6	ABX46316	Abx46316
50.0	30	6	ABA81781	PCR prime	c 173	13.8	49.3	53	6	ABL58495	Ab158495
50.0	31	6	ABQ76912	hdm2 proc	c 174	13.8	49.3	54	3	Aaa73940	Aaa73940
50.0	32	2	AAV55524	G-CSF cat	c 175	13.8	49.3	55	7	ABV99721	Abv99721
50.0	35	3	AAZ99392	PCR prime	c 176	13.8	49.3	55	3	Aaz96977	Aaz96977
50.0	35	6	ABQ73453	Human bet	c 177	13.8	49.3	60	6	ABK15020	Abk15020
50.0	35	6	ABQ73481	Human bet	c 178	13.8	49.3	60	6	ABN39954	Abn39954
50.0	38	2	AA747983	Cytomegal	c 179	13.8	49.3	60	6	ABN32494	Abn32494
50.0	38	2	AAV72563	Cytomegal	c 180	13.8	49.3	60	6	ABN37758	Abn37758
50.0	38	2	ABX75270	Human pol	c 181	13.8	49.3	60	6	ABN33459	Abn33459
50.0	39	6	ABS61182	Human gen	c 182	13.8	49.3	60	6	ABN38311	Abn38311
50.0	41	7	ABX75270	Human gen	c 183	13.8	49.3	60	6	ABN43288	Abn43288
50.0	47	4	AAH88415	CNS disor	c 184	13.6	48.6	20	7	ABK88103	Abk88103
50.0	50	6	AA145416	Coalt-de	c 185	13.6	48.6	20	7	ABZ77225	Abz77225
50.0	51	3	AA29133	Primer 2	c 186	13.6	48.6	21	6	AAZ31429	Aaz31429
50.0	51	4	AA178261	Human sil	c 187	13.6	48.6	23	2	AAZ06595	Aaz06595
50.0	51	4	AA178260	Human sil	c 188	13.6	48.6	23	2	AAF76641	Aaf76641
50.0	51	5	ABL00695	Human sil	c 189	13.6	48.6	24	2	Aax84498	Aax84498
50.0	52	4	AAH36992	Human col	c 190	13.6	48.6	24	7	ADA68190	Ada68190
50.0	55	3	AAH60852	AS-DHFR-G	c 191	13.6	48.6	25	4	AAF77678	Aaf77678
50.0	55	3	AA60851	AS-DHFR-G	c 192	13.6	48.6	25	6	ABN03112	Abn03112
50.0	60	2	AAZ09720	S. cerevi	c 193	13.6	48.6	25	6	ABN03113	Abn03113
50.0	60	2	AAZ09720	S. cerevi	c 194	13.6	48.6	25	6	ABN03108	Abn03108
50.0	60	4	AA29121	Oligonuc1	c 195	13.6	48.6	25	6	ABN03111	Abn03111
50.0	60	6	ABN47111	Human spl	c 196	13.6	48.6	25	6	ABN03109	Abn03109
50.0	60	6	ABN36352	Human spl	c 197	13.6	48.6	25	6	ABN03110	Abn03110
50.0	60	6	ABN34936	Human spl	c 198	13.6	48.6	25	8	ACK08595	Ack08595
50.0	60	6	ABN39579	Human spl	c 199	13.6	48.6	25	8	ACI08923	Ac108923
49.3	17	7	ACD50464	HBV hamme	c 200	13.6	48.6	25	8	ACI86360	Ac186360
49.3	20	4	AA545673	Human PAR	c 201	13.6	48.6	25	8	ACI55819	Ac155819
49.3	21	2	AAV31343	Phosphati	c 202	13.6	48.6	25	8	ACI43265	Ac143265
49.3	21	2	AAV15935	PCR prime	c 203	13.6	48.6	27	9	ADE47816	Ade47816
49.3	21	3	AAZ32885	Human PI	c 204	13.6	48.6	28	2	AAZ90109	Aaz90109
49.3	27	2	AAZ27093	Saccharom	c 205	13.6	48.6	30	6	ABX69917	Abx69917
49.3	29	2	AAV22304	Phosphoro	c 206	13.6	48.6	31	2	AAZ98805	Aaz98805
49.3	30	6	ABX68692	Novel Hel	c 207	13.6	48.6	34	2	AAZ85573	Aaz85573
49.3	32	2	AAZ06626	Brassica	c 208	13.6	48.6	36	9	ADC02784	Adc02784
49.3	32	3	AAZ51127	B. napus	c 209	13.6	48.6	36	9	ADC02786	Adc02786
49.3	34	3	AAZ56914	Human col	c 210	13.6	48.6	39	9	ADC24169	Adc24169
49.3	34	6	ABT12336	Orestes s	c 211	13.6	48.6	39	9	ADC24170	Adc24170
49.3	34	7	ACD91630	Human col	c 212	13.6	48.6	41	8	ACC42053	Acc42053
49.3	35	3	AAZ79948	PCR prime	c 213	13.6	48.6	42	3	AAZ05624	Aaz05624
49.3	35	4	AAZ03369	Reverse P	c 214	13.6	48.6	43	3	AAA60442	Aaa60442
49.3	41	2	AAZ56925	Human col	c 215	13.6	48.6	43	9	ADC24948	Adc24948
49.3	46	6	ABT12347	Orestes s	c 216	13.6	48.6	44	2	AAZ97219	Aaz97219
49.3	46	7	ACD91641	Human col	c 217	13.6	48.6	45	8	ADA73846	Ada73846
49.3	50	2	AAZ06722	HBV LLA2	c 218	13.6	48.6	45	8	ADA02300	Ada02300
49.3	50	4	AAZ33875	Human SNP	c 219	13.6	48.6	45	9	ADB72039	Adb72039
49.3	50	4	AAZ28618	Human SNP	c 220	13.6	48.6	47	3	AAZ67025	Aaz67025
49.3	50	4	AAH79788	Human DNA	c 221	13.6	48.6	47	3	AAZ22938	Aaz22938
49.3	50	6	ABZ04325	Human leu	c 222	13.6	48.6	51	5	ABL00814	Ab100814
49.3	50	6	ABZ07047	Human leu	c 223	13.6	48.6	54	3	AAA60434	Aaa60434
49.3	50	6	ABZ06231	Human leu	c 224	13.6	48.6	57	2	AAZ20589	Aaz20589
49.3	50	6	ABZ06657	Human leu	c 225	13.6	48.6	60	6	ABN38383	Abn38383
49.3	51	2	AAV19093	Synthetic	c 226	13.6	48.6	60	6	ABN38598	Abn38598
49.3	51	2	AAV1997	PCR prime	c 227	13.6	48.6	60	6	ABN39145	Abn39145
49.3	51	4	AAZ27306	Human SNP	c 228	13.6	48.6	60	6	ABN33262	Abn33262
49.3	51	4	AAZ27331	Human SNP	c 229	13.6	48.6	60	6	ABN40951	Abn40951
49.3	52	2	AAZ62204	Sindbis/H	c 230	13.6	48.6	60	6	ABN46279	Abn46279
49.3	52	2	AAZ31151	HDV rever	c 231	13.4	47.9	17	7	ACD51872	Ac51872
49.3	52	2	AAZ30817	HDV riboz	c 232	13.4	47.9	17	7	ACD51871	Ac51871
49.3	52	2	AAV42394	Nested PC	c 233	13.4	47.9	20	5	AAF54564	Aaf54564
49.3	52	2	AAV42426	Forward P	c 234	13.4	47.9	24	7	ABZ22957	Abz22957
49.3	52	2	AAV60154	Nested PC	c 235	13.4	47.9	25	2	AAZ46859	Aaz46859
49.3	52	2	AAV60185	Reverse P	c 236	13.4	47.9	25	2	AAT86146	Aat86146
49.3	52	2	AAV70746	Reverse P	c 237	13.4	47.9	25	8	ACI09244	Ac109244
49.3	52	2	AAV70714	Nested pr	c 238	13.4	47.9	26	2	AAT08624	Aat08624
49.3	52	3	AAZ92930	Hepatitis	c 239	13.4	47.9	27	2	AAQ40996	Aaq40996
49.3	52	3	AAZ92970	Hepatitis	c 240	13.4	47.9	27	2	AAQ40995	Aaq40995
49.3	52	3	AAZ92843	Hepatitis	c 241	13.4	47.9	27	2	AAV95527	Aav95527
49.3	52	3	AAZ92803	Hepatitis	c 242	13.4	47.9	27	2	AAZ08985	Aaz08985
49.3	52	6	AAZ38850	Alphaviru	c 243	13.4	47.9	27	2	AAZ08985	Aaz08985

46.4	29	6	ABN85372	Abn85372 Spumaretr	462	12.8	45.7	25	3	AAx82992	AAx82992
46.4	29	9	ADD22842	Add22842 Filamento	463	12.8	45.7	25	4	AAH21680	AAH21680
46.4	30	2	Az07825	Aaz07825 Oligo HRP	464	12.8	45.7	25	4	AAH21688	AAH21688
46.4	31	7	ACD43774	Acd43774 Human gpn	465	12.8	45.7	25	4	AAH37767	AAH37767
46.4	32	8	ABZ81516	Abz81516 Human gpn	466	12.8	45.7	25	4	AAH10619	AAH10619
46.4	33	3	AAA61420	Aaa61420 Human gly	467	12.8	45.7	25	6	ABV85910	ABV85910
46.4	35	7	AAAD48346	Aaad48346 S. cerevi	468	12.8	45.7	25	6	ABV85911	ABV85911
46.4	40	2	AAQ55601	Aaq55601 Flanking	C 469	12.8	45.7	25	6	ABV91561	ABV91561
46.4	41	2	AAV47777	Aav47777 Maize pol	C 470	12.8	45.7	25	6	ABV91560	ABV91560
46.4	41	2	AAV47777	Aav47777 Maize pol	471	12.8	45.7	25	7	ABD02934	ABD02934
46.4	41	6	ABZ47636	Abz47636 Human ATP	472	12.8	45.7	25	7	ABD02935	ABD02935
46.4	41	6	ABZ45513	Abz45513 Human ATP	473	12.8	45.7	25	8	ACK09539	ACK09539
46.4	41	6	ABZ45041	Abz45041 Human ATP	C 474	12.8	45.7	25	8	ACT190732	ACT190732
46.4	41	6	ABZ43334	Abz43334 Human N-m	C 475	12.8	45.7	26	3	AAA93717	AAA93717
46.4	41	6	ABZ48674	Abz48674 Human N-m	C 476	12.8	45.7	26	6	ABK67133	ABK67133
46.4	41	6	ABZ46919	Abz46919 Human ATP	C 477	12.8	45.7	26	6	ABK12970	ABK12970
46.4	41	9	AAJ55682	Aaj55682 Human Na/	C 478	12.8	45.7	27	2	AAK63179	AAK63179
46.4	42	2	ABV10835	Aav10835 Human MSH	C 479	12.8	45.7	27	2	AAV98130	AAV98130
46.4	42	6	ABL01835	Abi01835 HNSH2 pre	480	12.8	45.7	29	2	AAQ44286	AAQ44286
46.4	44	7	ABQ80068	Abq80068 T. mariti	481	12.8	45.7	29	2	AAQ42344	AAQ42344
46.4	45	2	AAQ66712	Aaq66712 Primer to	C 482	12.8	45.7	29	2	AAT18889	AAT18889
46.4	47	3	Az65736	Aaz65736 Human map	C 483	12.8	45.7	29	4	AAC97091	AAC97091
46.4	48	8	AAJ62163	Aaj62163 Human IL-	C 484	12.8	45.7	29	4	AC971164	AC971164
46.4	49	3	AAZ46880	Aaz46880 Human MLH	C 485	12.8	45.7	29	7	ABT15536	ABT15536
46.4	50	6	ABZ06157	Abz06157 Human leu	486	12.8	45.7	30	2	AQ52012	AQ52012
46.4	50	6	ABZ02986	Abz02986 Human leu	487	12.8	45.7	30	2	AQ73658	AQ73658
46.4	50	6	ABZ07651	Abz07651 Human leu	488	12.8	45.7	30	2	AAT33576	AAT33576
46.4	51	4	AAJ32903	Aaj32903 Human SNP	C 490	12.8	45.7	30	2	AAT29635	AAT29635
46.4	51	4	AAJ75897	Aaj75897 Human sli	C 491	12.8	45.7	30	2	AAV75149	AAV75149
46.4	51	4	AAH90525	Aah90525 Human cto	C 492	12.8	45.7	30	6	AAV64108	AAV64108
46.4	54	3	AAZ73942	Aaz73942 GFP ile/A	C 493	12.8	45.7	30	6	ABX69054	ABX69054
46.4	58	3	AAZ29736	Aaz29736 Primer-2	C 494	12.8	45.7	30	8	ABA93865	ABA93865
46.4	58	7	ACA89879	Aca89879 Human IL-	C 495	12.8	45.7	31	3	ACD27622	ACD27622
46.4	58	7	ACA89879	Aca89879 Human IL-	C 496	12.8	45.7	32	6	AAH78753	AAH78753
46.4	58	7	ACA84663	Aca84663 Human int	C 497	12.8	45.7	32	6	AAJ17090	AAJ17090
46.4	58	8	ADA43262	Ada43262 Human int	C 498	12.8	45.7	32	6	AAJ20633	AAJ20633
46.4	58	8	ADA49803	Ada49803 Human int	C 499	12.8	45.7	33	4	AAQ00367	AAQ00367
46.4	58	9	ADA26997	Ada26997 Human IL-	C 500	12.8	45.7	33	5	AAQ69053	AAQ69053
46.4	58	9	ADB66930	Adb66930 Human PRO	501	12.8	45.7	33	6	AAH48364	AAH48364
46.4	60	6	ABN47374	Abn47374 Human spl	C 502	12.8	45.7	33	6	ABQ77965	ABQ77965
46.4	60	6	ABN44408	Abn44408 Human spl	C 503	12.8	45.7	33	6	AAJ53835	AAJ53835
46.4	60	6	ABN42474	Abn42474 Human spl	C 504	12.8	45.7	33	7	ABK49118	ABK49118
46.4	60	6	ABN35722	Abn35722 Human spl	C 505	12.8	45.7	36	4	ACF06227	ACF06227
46.4	60	6	ABN45654	Abn45654 Human spl	C 506	12.8	45.7	36	4	AAG77835	AAG77835
46.4	60	6	ABN40427	Abn40427 Human spl	C 507	12.8	45.7	36	4	AAH50206	AAH50206
46.4	60	6	ABN42615	Abn42615 Human spl	C 508	12.8	45.7	36	7	ACD26342	ACD26342
46.4	60	6	ABN32591	Abn32591 Human spl	C 509	12.8	45.7	37	3	Aaz38564	Aaz38564
46.4	60	6	ABN44580	Abn44580 Human spl	510	12.8	45.7	38	2	AAZ38564	AAZ38564
46.4	60	6	ABN35306	Abn35306 Human spl	511	12.8	45.7	38	2	AAJ81030	AAJ81030
46.4	60	6	ABN45676	Abn45676 Human spl	C 512	12.8	45.7	38	8	ACC99668	ACC99668
46.4	60	6	ABN46934	Abn46934 Human spl	C 513	12.8	45.7	38	8	ACC99674	ACC99674
46.4	60	6	ABN42615	Abn42615 Human tum	C 514	12.8	45.7	41	7	ABZ32747	ABZ32747
46.4	60	6	ABN42615	Abn42615 HCV DNaz	C 515	12.8	45.7	41	7	ABZ25886	ABZ25886
46.4	60	6	ABN42615	Abn42615 HBV hamme	C 516	12.8	45.7	41	7	ABZ70734	ABZ70734
46.4	60	6	ABN42615	Abn42615 Forward R	C 517	12.8	45.7	42	2	AAQ75448	AAQ75448
46.4	60	6	ABN42615	Abn42615 Human bia	C 518	12.8	45.7	42	6	ABK13824	ABK13824
46.4	60	6	ABN42615	Abn42615 Human TAP	519	12.8	45.7	43	2	AAQ53774	AAQ53774
46.4	60	6	ABN42615	Abn42615 HLA Class	C 520	12.8	45.7	43	2	AAQ75450	AAQ75450
46.4	60	6	ABN42615	Abn42615 Human ABC	521	12.8	45.7	43	2	AAT07975	AAT07975
46.4	60	6	ABN42615	Abn42615 Human ABC	522	12.8	45.7	43	2	AAV00991	AAV00991
46.4	60	6	ABN42615	Abn42615 TNFR1 exp	523	12.8	45.7	43	2	AAV14776	AAV14776
46.4	60	6	ABN42615	Abn42615 Bovine FM	524	12.8	45.7	43	2	AAV79851	AAV79851
46.4	60	6	ABN42615	Abn42615 Molecular	525	12.8	45.7	43	3	AAA92951	AAA92951
46.4	60	6	ABN42615	Abn42615 Zea mays	526	12.8	45.7	43	6	ABK61327	ABK61327
46.4	60	6	ABN42615	Abn42615 Replicati	527	12.8	45.7	43	6	AAJ80088	AAJ80088
46.4	60	6	ABN42615	Abn42615 Human pap	528	12.8	45.7	45	3	AAJ58514	AAJ58514
46.4	60	6	ABN42615	Abn42615 Human pap	529	12.8	45.7	45	3	AAJ01258	AAJ01258
46.4	60	6	ABN42615	Abn42615 Cytomegal	530	12.8	45.7	45	3	AAA49494	AAA49494
46.4	60	6	ABN42615	Abn42615 CMV MIE g	531	12.8	45.7	45	3	AAA46913	AAA46913
46.4	60	6	ABN42615	Abn42615 hCMV Prim	C 532	12.8	45.7	45	5	AAH26512	AAH26512
46.4	60	6	ABN42615	Abn42615 Cytomegal	533	12.8	45.7	45	7	ABX75476	ABX75476
46.4	60	6	ABN42615	Abn42615 CMV innmed	534	12.8	45.7	45	7	ABX89467	ABX89467

44.3	32	2	AAT78674	Rat78674 Primer 5p	900	12.4	44.3	41	6	ABZ47942
44.3	32	2	AAT87102	Aat87102 SELEX PCR	C 901	12.4	44.3	41	6	ABZ45805
44.3	32	2	AAT19550	Aat19550 Complemen	C 902	12.4	44.3	41	6	ABZ46151
44.3	32	2	AAT31104	Aat31104 SELEX PCR	C 903	12.4	44.3	41	6	ABZ50218
44.3	32	3	AAT52789	Aat52789 PCR prime	904	12.4	44.3	41	6	ABZ45595
44.3	32	3	AAZ40148	C. tetani	905	12.4	44.3	41	7	ABX50132
44.3	32	3	AAC69845	Aac69845 SELEX PCR	C 906	12.4	44.3	41	7	ABX75154
44.3	32	4	AAC69864	Aac69864 40N7a ssd	907	12.4	44.3	41	8	ACD27787
44.3	32	4	AAT70637	Aat70637 SELEX exp	908	12.4	44.3	41	8	ACD40547
44.3	32	5	AAT90705	Aat90705 SELEX PCR	C 909	12.4	44.3	42	2	AAV57974
44.3	32	6	ABL41378	Human G-s	C 910	12.4	44.3	42	2	AAV10877
44.3	32	6	ABL57272	5N7 prime	C 911	12.4	44.3	42	3	AAA07291
44.3	32	8	ADA21795	Ada21795 HGF 30N7	912	12.4	44.3	42	4	AAQ13783
44.3	33	2	AAT78601	Aat78601 Primer #1	913	12.4	44.3	42	4	AAQ45693
44.3	33	2	AAX89097	Aax89097 SXR direc	C 914	12.4	44.3	43	2	AAV71144
44.3	33	3	AAX89096	Aax89096 SXR direc	915	12.4	44.3	43	2	AAV12572
44.3	33	5	AAX25506	Aah25506 Steroid-a	916	12.4	44.3	43	2	AAV26870
44.3	33	5	AAX25507	Aah25507 Steroid-a	C 917	12.4	44.3	43	2	AAV27603
44.3	33	6	ABQ83892	Abq83892 Human mac	C 918	12.4	44.3	43	6	AAJ30589
44.3	33	6	AB199977	Abi199977 Human dea	C 919	12.4	44.3	44	3	AAA98736
44.3	33	7	AAD50130	Aad50130 SXR respo	C 921	12.4	44.3	44	3	AAA28462
44.3	33	8	ACD27784	SXR DNA b	922	12.4	44.3	44	7	AAQ72666
44.3	33	8	ACD27785	SXR DNA b	923	12.4	44.3	44	7	AAQ80082
44.3	33	8	ACD40544	Direct re	924	12.4	44.3	45	2	AAK58007
44.3	34	3	AAA75581	Aaa75581 PCR prime	C 925	12.4	44.3	45	2	AAK51403
44.3	34	6	AAS20689	Aas20689 Mouse zal	C 926	12.4	44.3	46	6	ABQ96530
44.3	35	2	AAQ54464	Aaq54464 Mycoplasm	C 927	12.4	44.3	46	6	ABK96282
44.3	35	2	AAQ54183	Aat45183 Mycoplasm	C 928	12.4	44.3	47	6	ABK96282
44.3	35	2	AAT45163	Aat45163 Mycoplasm	C 929	12.4	44.3	49	9	ADK99551
44.3	35	2	AAT49334	Aav49334 Primer AB	C 930	12.4	44.3	50	2	AAQ50268
44.3	36	2	AAX89098	Aax89098 SXR direc	931	12.4	44.3	50	2	AAH74727
44.3	36	3	AAA28459	Aaa28459 Oligonucle	932	12.4	44.3	50	4	AAH26885
44.3	36	3	AAA46527	Aaa46527 PCR prime	933	12.4	44.3	50	4	AAH45616
44.3	36	5	AAD25508	Aah25508 Steroid-a	935	12.4	44.3	50	6	AAH24217
44.3	36	8	ACD27786	Direct re	C 937	12.4	44.3	51	2	AAH4793
44.3	36	8	ACD40546	Direct re	C 938	12.4	44.3	51	4	AAH27751
44.3	37	3	AAT70159	T7 promot	C 940	12.4	44.3	51	4	AAH27390
44.3	37	4	AAH25817	Aah25817 Human/mou	941	12.4	44.3	51	4	AAH27390
44.3	38	4	ABK04754	Abk04754 Human NOG	C 942	12.4	44.3	51	4	AAH27366
44.3	38	7	ACD50514	ACD50514 HBV hamme	C 943	12.4	44.3	51	4	AAH27366
44.3	38	7	ACD52458	ACD52458 HBV inozy	C 944	12.4	44.3	51	4	AAH27366
44.3	39	7	ACF56962	ACF56962 DGI-3 PCR	C 945	12.4	44.3	51	4	AAH27366
44.3	40	2	AAT14232	Primer 5p	C 946	12.4	44.3	51	4	AAH27366
44.3	40	2	AAT42817	Aat42817 Primer #3	C 947	12.4	44.3	51	4	AAH27366
44.3	40	2	AAT87104	Aat87104 Primer 5p	C 948	12.4	44.3	51	4	AAH27366
44.3	40	2	AAX85061	Aax85061 PCR prime	949	12.4	44.3	51	4	AAH27366
44.3	40	6	ABT12259	ABT12259 E coli ex	950	12.4	44.3	51	5	AAH27366
44.3	40	6	ABT12254	ABT12254 E coli ex	C 952	12.4	44.3	51	5	AAH27366
44.3	40	6	ABT122114	ABT122114 E coli ex	C 953	12.4	44.3	52	4	AAH27366
44.3	40	7	ACC43714	Acc43714 PCR prime	C 954	12.4	44.3	52	4	AAH27366
44.3	40	7	ADA48879	Ada48879 PCR prime	C 955	12.4	44.3	52	4	AAH27366
44.3	41	2	ABQ80076	Abq80076 T. mariti	C 956	12.4	44.3	52	7	ADA47349
44.3	41	2	AAT35888	Aat35888 Marek Dis	957	12.4	44.3	53	2	AAZ10169
44.3	41	2	AAT39323	Primer CD	C 958	12.4	44.3	53	6	AAZ10169
44.3	41	2	AAT35920	Aat35920 Marek Dis	C 959	12.4	44.3	54	2	AAZ10169
44.3	41	2	AAV42533	Aav42533 PCR prime	C 960	12.4	44.3	54	9	ABX94281
44.3	41	2	AAX89099	Aax89099 SXR direc	C 961	12.4	44.3	54	9	ABX94281
44.3	41	3	AAZ61052	AAZ61052 PCR prime	C 962	12.4	44.3	56	2	AAZ10169
44.3	41	5	AAH25509	Aah25509 Steroid-a	963	12.4	44.3	57	3	AAQ63713
44.3	41	5	AAH48366	Aah48366 Aldehyde-	964	12.4	44.3	57	3	AAQ63713
44.3	41	6	ABZ72301	Gene 216	C 965	12.4	44.3	58	3	AAZ15196
44.3	41	6	ABK47539	Abk47539 Avidin 9	C 966	12.4	44.3	58	3	AAZ15196
44.3	41	6	ABZ70769	Abz70769 Human zin	C 967	12.4	44.3	59	4	AAH26556
44.3	41	6	ABZ45596	Human ATP	968	12.4	44.3	59	4	AAH26556
44.3	41	6	ABZ47941	Human ATP	969	12.4	44.3	60	2	AAH26556
44.3	41	6	ABZ47941	Human ATP	C 971	12.4	44.3	60	2	AAH26556
44.3	41	6	ABZ47941	Human ATP	C 972	12.4	44.3	60	6	AAH26556
44.3	41	6	ABZ47941	Human ATP	C 972	12.4	44.3	60	6	AAH26556

44.3 60 6 ABN36828 Human spl
 44.3 60 6 ABN35852 Human spl
 44.3 60 6 ABN38394 Human spl
 44.3 60 6 ABN40449 Human spl
 44.3 60 6 ABN32230 Human spl
 44.3 60 6 ABN58873 Human spl
 44.3 60 6 ABN32787 Human spl
 44.3 60 6 ABN42207 Human spl
 44.3 60 6 ABN36167 Human spl
 44.3 60 6 ABN34404 Human spl
 44.3 60 6 ABN44236 Human spl
 44.3 60 6 ABN39531 Human spl
 44.3 60 6 ABN43076 Human spl
 44.3 60 6 ABN58663 Human spl
 44.3 60 6 ABN35048 Human spl
 44.3 60 6 ABN45323 Human spl
 44.3 60 6 ABN39998 Human spl
 44.3 60 7 ACD07797 Human spl
 43.6 17 3 AAF07343 Human spl
 43.6 17 7 ABT34426 Human spl
 43.6 17 7 ACC64892 Human spl
 43.6 17 9 ADC04115 Human spl
 43.6 18 4 AAH77481 Human spl
 43.6 19 6 ABK33800 Human inh
 43.6 19 6 ABS59907 Human inh
 43.6 20 2 AAQ39568 Human inh
 43.6 20 2 AAV26799 Human inh
 43.6 20 2 AAX80916 Human inh

ALIGNMENTS

standard; DNA; 28 BP.

2 (first entry)

ontrol probe SEQ ID NO:23.

; carcinoembryonic antigen; adenocarcinoma; oesophagus;
 ; probe; ss.

1-A1.

2.

2; 2002WO-US006504.

1; 2001US-0273277P.

IV PITTSBURGH.

; Luketich JD, Raja S, Kelly LA, Finkelstein SD;

732795/79.

PCR method for detecting malignancies, e.g. adenocarcinoma of
 gus comprises conducting a PCR amplification on a DNA sample in
 tion mixture.

Page 78; 141pp; English.

it invention describes a multiplex polymerase chain reaction
 comprising conducting PCR on a DNA sample in a reaction
 conducted in first and second amplification stages, each with one
 R cycles comprising denaturing, annealing and elongating steps
 elongating step may be conducted at the same temperature as the

CC annealing step. The second amplification stage of (M1) is conda
 CC different reaction conditions from that of the first amplifica
 CC to modulate the relative rate of production of the first ampli
 CC first primer set and a second amplicon by a second primer set
 CC first and second amplification stages. Also described: (1) an
 CC oligonucleotide comprising 15-28 bp or its derivative; (2) int
 CC PCR diagnostic; (3) rapid detection of a malignancy or of meta
 CC adenocarcinoma of the oesophagus; or (4) a cartridge for use i
 CC automated PCR system. (M1) is useful for detecting malignancie
 CC adenocarcinoma of the oesophagus. (M1) eliminates contaminatio
 CC decreases the time it takes to carry out a PCR reaction. The p
 CC sequence represents an internal control probe, which is used i
 CC example from the present invention

XX Sequence 28 BP; 6 A; 8 C; 6 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 28; DB 6; Length 28;

Best Local Similarity 100.0%; Pred. No. 0.021; Mismatches 0; Indels 0;

Matches 28; Conservative 0; Mismatches 0; Indels 0;

QY 1 AGCATCATCCTCTGCATGTCAGTGCAT 28

Db 1 AGCATCATCCTCTGCATGTCAGTGCAT 28

RESULT 2

AAV84287

ID AAV84287 standard; DNA; 20 BP.

XX AAV84287;

XX 12-APR-1999 (first entry)

XX LacZ reporter gene primer LacZP1.

XX Flk-1; endothelial growth factor receptor-2; VEGF; transcripti
 KW endothelium; enhancer; vascular disease; angiogenesis; cancer;
 KW diabetic retinopathy; rheumatoid arthritis; wound healing; vul
 KW atherosclerosis; tumour; neuronal disorder; therapy; diagnosis
 KW PCR; primer; lacZ; reporter gene; ss.

OS Synthetic

XX WO9855638-A1

XX 10-DEC-1998

XX 03-JUN-1998; 98WO-EP003318.

XX 03-JUN-1997; 97EP-00108959.

XX (PLAC) MAX FLANCK GRS FOERDERUNG WISSENSCHAFTEN.

XX Breier G, Risau W, Roenicke V;

XX WPI; 1999-059915/05.

XX New recombinant DNA containing heterologous sequence controlle

XX endothelial cell specific regulator - from the Flk-1 gene, use

XX prevent or diagnose vascular disease, tumours, also to screen

XX transcriptional regulators.

XX Example 10; Page 48; 107pp; English.

XX This is the nucleotide sequence of primer LacZP1, which was us

XX primer LacZP2 (see AAV84288) in a PCR analysis for genotyping

XX knock-in mouse embryos, in which the lacZ gene was under contr

XX regulatory elements from the 5' untranslated region (5'-UTR, s

XX AAV84274) of the murine endothelial growth factor receptor-2 g

XX Complete vascular staining of Flk-1/lacZ knock-in embryos at E

XX indicated that the 5'-UTR is not essential for vascular expres

XX embryo proper. However, the 5'-UTR is required for expression

XX the yolk sac vasculature. The invention provides a new claimed

5 DNA comprising at least one regulatory sequence from an the Flk-1 gene that controls expression in endothelial cells, and which is linked to a heterologous DNA. Such constructs, comprising them, are used to produce pharmaceutical compositions ng, preventing and/or delaying vascular and tumorous diseases

0 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

71.4%; Score 20; DB 2; Length 20;

Similarity 100.0%; Pred. No. 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TCCTCTGCATGTCAGGTC 26

TCCTCTGCATGTCAGGTC 20

standard; DNA; 20 BP.

2 (first entry)

a domain-containing fusion protein-related PCR primer 29.

tein; recombinase domain; signal peptide domain; gene function; port; recombinase recognition sequence; transgenic organism; combination system; site-specific integration; gene therapy; r; ss.

ed.

3-A2.

2.

1; 2001WO-EP012975.

0; 2000EP-00124629.

1; 2001EP-00109543.

1; 2001US-0311876P.

TEMIS PHARM GMBH.

Felder S, Schwenk F, Kueter-Luks B, Faust N;

319298/55.

on protein useful for recombining DNA molecules in eukaryotic recombinase protein which is linked to signal peptide domain its nuclear import of fusion protein in eucaryotic cells.

Page 131; 150pp; English.

ion comprises the amino acid and coding sequences of fusion at contain a recombinase domain and a signal peptide domain its nuclear import of the fusion protein in eukaryotic cells. proteins of the invention are useful for recombining the DNA of cells or organisms containing recombinase recognition for the recombinase domain of the fusion proteins. The fusion f the invention are useful for studying gene function at velopmental stages and for the creation of transgenic The C31-Int recombination system of the invention can be used e-specific integration of foreign DNA into the genome of cells (e.g. for gene therapy). The present DNA sequence a PCR primer that was used in the invention

0 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

71.4%; Score 20; DB 6; Length 20;

Similarity 100.0%; Pred. No. 52;

Matches 20; Conservative 0; Mismatches 0; Indels 0;

QY 7 ATCCTCTGCATGTCAGGTC 26

Db 1 ATCCTCTGCATGTCAGGTC 20

RESULT 4

ADB81355

ID ADB81355 standard; DNA; 20 BP.

XX ADB81355;

XX ADB81355;

DT 04-DEC-2003 (first entry)

XX PCR primer beta-Gal 3 to amplify the ROSA26-C31 reporter allele

XX PCR; ss; phiC31 integrase; site specific recombinase; SSR; gen disease model; gene therapy; transgenic; C31-Int; primer; reporter allele; ROSA26-C31; LacZ; beta-Gal 3.

XX Unidentified.

XX WO2003066867-A2.

XX 14-AUG-2003.

XX 05-FEB-2003; 2003WO-EP001122.

XX 06-FEB-2002; 2002US-0354741P.

XX (ARTE-) ARTEMIS PHARM GMBH.

XX Andreas S, Faust N;

XX WPI; 2003-663599/62.

XX New genetically engineered nucleic acid molecule, useful for p agent for recombining a DNA molecule containing phiC31 integra recognition sequences in a eukaryotic cell, a vertebrate or tr organism.

Example 3; Page 87; 87pp; English.

XX This invention relates to novel genetically engineered nucleic CC molecules encoding phiC31 integrase (C31-Int), which has been CC optimised for expression in eukaryotic host cells. The phiC31 CC is a site specific recombinase (SSR) that catalyzes recombina CC two phiC31 recognition sequences. The introduction of silent m CC into the coding sequence changes the given codon to one that i CC frequently used in the respective host, which in turn alters e CC levels. Accordingly, using this ability to generate controlled CC permanent modifications in eukaryotic genomes has various rese CC applications including the study of gene function and the crea CC disease models, as well as gene therapy for medical applica CC design of economically important animals and crops. Furthermore CC phiC31 integrase of the invention is useful for preparing an a CC recombining a DNA molecule containing phiC31 integrase recogni CC sequences in a eukaryotic cell, a vertebrate or transgenic org CC oligonucleotide sequence is the PCR primer designated beta-Gal CC is used to amplify the ROSA26-C31 reporter allele (LacZ) in an CC exemplification of the invention.

SQ Sequence 20 BP; 3 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 71.4%; Score 20; DB 9; Length 20;

Best Local Similarity 100.0%; Pred. No. 52;

Matches 20; Conservative 0; Mismatches 0; Indels 0;

QY 7 ATCCTCTGCATGTCAGGTC 26

Db 1 ATCCTCTGCATGTCAGGTC 20

standard; DNA; 19 BP.

19 (first entry)

specific primer.

endothelial growth factor; VEGF; mouse; hypoxia;
disease; tumour; cancer; angiogenesis; wound healing; therapy;
PCR; primer; lacZ gene; ss.

la coli.

-Al.

38.

38; 98WO-EP003517.

37; 97EP-00109418.

LX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

Damert A, Plate K;

-080911/07.

inant DNA - contains sequence that regulates hypoxia-induced
t, used for, e.g. treatment and diagnosis of vascular disease.

: Page 34; 80pp; English.

specific primers (see AAV82445 and AAV82446) were used to
transfect GS9L cells following transfection with constructs
of murine vascular endothelial growth factor (VEGF) gene
sequences as fusions to lacZ reporter genes. Experiments were
to determine hypoxia mediated expression of VEGF in vivo and in
invention relates to recombinant DNA molecules comprising
sequences of the VEGF gene, especially the 3' untranslated
region (see AAV82439) and promoter (see AAV82440), being capable of
inducible expression of a heterologous DNA in vivo.
abundant DNA molecules, vectors, host cells and transgenic
in be used to identify and develop compounds and methods for
treating, preventing and/or delaying a vascular or tumour

19 BP; 2 A; 6 C; 5 G; 6 T; 0 U; 0 Other;

67.9%; Score 19; DB 2; Length 19;

Similarity 100.0%; Pred. No. 1.4e+02;

: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TCCTGTCATGTCAGGTC 26

|||||

TCCTGTCATGTCAGGTC 19

standard; DNA; 30 BP.

39 (first entry)

a cysteine protease PCR primer pro-pst1441.

protease; barley; transgenic plant; disease resistance;

prevention; treatment; infection; stress; temperature; drought;
wound; root-specific expression; antimicrobial; antistress;
anti-wounding; PCR primer; ss.

Synthetic.

Hordeum vulgare.

WO9910500-A1.

04-MAR-1999.

21-AUG-1998; 98WO-EP005339.

26-AUG-1997; 97DE-01037118.

22-JAN-1998; 98DE-01002384.

(PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.

Schlichter U, Steinbiss H, Antoniw J;

WPI; 1999-204668/17.

Nucleic acid encoding plant cysteine protease - that increase;
to injury and infection.

Example 6; Page 72; 81pp; German.

This invention describes a novel Hordeum vulgare cysteine protease
is used to produce transgenic plants with (a) increased or re-
expression of protease or (b) increased resistance to disease
(particularly prevention or treatment of infection) or other;
factors such as extreme temperatures, drought, salt or wound;
invention also describes a regulatory region which is used to
root-specific expression of heterologous DNA following infect-
of roots. The products of the invention have antimicrobial, an-
and anti-wounding activity in plants

Sequence 30 BP; 4 A; 10 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 64.3%; Score 18; DB 2; Length 30;

Best Local Similarity 80.8%; Pred. No. 4e+02;

Matches 21; Conservative 0; Mismatches 5; Indels 0.

QY 3 CATCATCTCTGTCATGTCAGGTCAT 28

|||||

Db 3 CATCTTCATCTGCAGGTCAGGTCCT 28

RESULT 7

ABN50202

ID ABN50202 standard; DNA; 60 BP.

AC ABN50202;

DT 15-JUL-2002 (first entry)

DE Human spliced transcript detection oligonucleotide SEQ ID NO:;
Human; mouse; rat; splice transcript; detection; RNA transcrip-
splice variant; transcriptome; oligonucleotide library; ss.

OS Homo sapiens.

FN WO200210449-A2.

PD 07-FEB-2002.

PF 20-JUL-2001; 2001WO-IB001903.

PR 28-JUL-2000; 2000US-0221607P.

PR 02-MAY-2001; 2001US-0287724P.

PA (COMP-) COMPUEN INC.

Wasserman A, Mintz E, Mintz L, Faigler S;
257383/30.

ucleotide libraries comprising oligonucleotides which hybridize to mRNAs transcribed from a transcription unit of a gene. The libraries are useful for detecting tissue-, pathology-, and developmental- changes.

SEQ ID NO 22950; 47pp; English.

This invention describes oligonucleotide libraries for detecting RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple genes that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of RNAs transcribed from a given transcription unit of the genome. The library may include one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in identifying RNA transcripts and splice variants of human or animal genomes. The libraries may also be used as specialised mini-transcriptomes to detect transcripts of a sub-transcriptome under a particular biological or pathological state, and so allowing the detection of tissue or cell-type specific genes such as those genes only expressed in a particular tissue or under a specific pathological condition; to detect specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disease. The oligonucleotide libraries, such as those represented by ABN27252 to ABN59589 represent oligonucleotide sequences from human and mouse, which are used in the exemplification of the invention. N.B. The sequence data for this patent did not form part of the published specification, but was obtained in electronic format from WIGO at ftp.wigo.int/pub/published pct sequences

) BP; 13 A; 17 C; 15 G; 15 T; 0 U; 0 Other;

62.1%; Score 17.4; DB 6; Length 60;

Similarity 77.8%; Pred. No. 8.1e+02;
Conservative 0; Mismatches 6; Indels 0; Gaps 0;

28
 38
 28
 38

:andard; DNA: 40 BP.

; (first entry)

essible CpG deprived gene related oligo SEQ ID No 177.

Escherichia coli; expression; DNA vaccine; gene therapy; ds.

١٩٩

17.

2.

-; 2001FR-00003274.

-; 2001ER-00003274.

LA SARL.

'15203/78.

PT Preparing gene with no cytosine methylation, useful e.g. for e
PT proteins in *Escherichia coli*, by selecting codons to avoid pre
PT CpG dinucleotides.

PS Disclosure; Fig 10a; 152pp; French.

The invention relates to a method for preparing a gene that is still expressible in *Escherichia coli* by synthesis of a polynucleotide sequence, encoding a protein expressible in *E. coli* but lacking any of the stop codons NCG, CGN or NTA (N = any of A, C, G or T) or any codons in C when the following codon starts with G. The CpG lacking gene is especially useful as selection (antibiotic resistance) or marker gene, but they (also CpG-free promoters, transcription units, replication, plasmids and cells for replication of the plasmid used for transformation, for biotechnological or medical purposes) are particularly well suited for preparation of DNA vaccines in humans or animals. The polynucleotides of the invention can be used for treating disorders by gene therapy. This polynucleotide sequence represents an oligonucleotide relating to the *Escherichia coli* expressible CpG gene of the invention.

Sequence 40 BP; 5 A; 11 C; 12 G; 12 T; 0 U; 0 Other;

Query Match 61.4%; Score 17.2; DB 6; Length 40;

Best Local Similarity 86.4%; Pred. No. 9.2e+02;
Matches 19; Conservative 0; Mismatches 3; Indels 0;

QY 1 AGCATCATCCTCTGCATGGTCA 22

Db 23 AGCACCCCTCTGCATGGACA 2

RESULT 9

ABT12155
ID ABT12155 standard; DNA; 40 BP.

AC ABT12155;

DT 19-DEC-2002 (first entry)

DE E coli expressible CpG deprived gene related oligo SEQ ID No 1'

CpG; *Escherichia coli*; expression; DNA vaccine; gene therapy; KW

OS Unidentified.

PN FR2821855-A1.

PD 13-SEP-2002.

PF 09-MAR-2001;

PR 09-MAR-2001; 2001FR-00003274.

PA (CAYL-) CAYLA S.A.R.L.

WPI: 2002-715203/78

PT Preparing gene with

PT proteins in *Escherichia coli*, by selecting codons to avoid pre-
PT CoG dinucleotides.

XX PS Disclosure: Fig 10a; 152pp; French.

The invention relates to a method for preparing a gene that lac is still expressible in *Escherichia coli* by synthesis of a polypeptide sequence, encoding a protein expressible in *E. coli* but lacking codons NCG, CGN or NTA (N = any of A, C, G or T) or any codons in C when the following codon starts with G. The CPG lacking gene is especially useful as selection (antibiotic resistance) or marker genes, but they (also CPG-free promoters, transcription units, replication, plasmids and cells for replication of the plasmids) can be used for transformation, for biotechnological or medical purposes.

articularly well suited for preparation of DNA vaccines for use or animals. The polynucleotides of the invention can be used in disorders by gene therapy. This polynucleotide sequence an oligonucleotide relating to the *Escherichia coli* e CpG gene of the invention

0 BP; 14 A; 10 C; 9 G; 7 T; 0 U; 0 Other;

60.7%; Score 17; DB 6; Length 40;

Similarity 80.0%; Pred. No. 1.1e+03;

Conservative 0; Mismatches 5; Indels 0; Gaps 0;

TCATCTCTGTCAGTGCAGTGCAT 28

||||| ||||| ||||| ||||| |||||

CCACCTCTGCAATGACAGTGCAT 25

standard; DNA; 60 BP.

2 (first entry)

ded transcript detection oligonucleotide SEQ ID NO:21137.

se; rat; splice transcript; detection; RNA transcript; iant; transcriptome; oligonucleotide library; ss.

ns.

9-A2.

2.

1; 2001WO-IB001903.

0; 2000US-0221607P.

1; 2001US-0257724P.

MPUGEN INC.

Wasserman A, Mintz E, Mintz L, Faigler S;

257383/30.

ucleotide libraries comprising oligonucleotides which y hybridize to mRNAs transcribed from a transcription unit of a eful for detecting tissue-, pathology-, and developmental- enes.

SEQ ID NO 21137; 47pp; English.

t invention describes oligonucleotide libraries for detecting RNAs that populate a (sub-)transcriptome, where the (sub-)ome comprises messenger RNAs transcribed from multiple ion units that populate a genome. The library comprises several oxides, each capable of hybridizing selectively to a set of RNAs transcribed from a given transcription unit of the genome, des one or more messenger RNA splice variants. The oride libraries are useful for detecting mRNAs from a sample, in expression profiling studies, in qualitatively or vely characterizing the corresponding transcriptome, and in RNA transcripts and splice variants of human or animal ome. The libraries may also be used as specialised mini to detect transcripts of a sub-transcriptome under a particular or pathological state, and so allowing the detection of tissue ology-specific genes such as those genes only expressed in issue under a specific pathological condition; to detect tal specific genes; and to detect RNA transcripts and splice f a transcriptome of a patient suffering from a particular ABN27253 to ABN59589 represent oligonucleotide sequences from

CC rats, humans and mice, which are used in the exemplification c
CC present invention. N.B. The sequence data for this patent did
CC part of the printed specification, but was obtained in electr
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 60 BP; 14 A; 14 C; 18 G; 14 T; 0 U; 0 Other;

Query Match 60.0%; Score 16.8; DB 6; Length 60;

Best Local Similarity 75.0%; Pred. No. 1.5e+03;

Matches 21; Conservative 0; Mismatches 7; Indels 0;

QY 1 AGCATCATCTCTGTCAGTGCAGTGCAT 28

||||| ||||| ||||| ||||| |||||

Db 7 ACCATCATCCAGAGCTTGGCGAGGTGAT 34

RESULT 11

AAQ51481

ID AAQ51481 standard; DNA; 29 BP.

XX

AC AAQ51481;

XX

DT 25-MAR-2003 (revised)

DT 16-MAY-1994 (first entry)

XX

DE Dengue virus sequence primer (pMAL-CRI/NS2-1 - DIR-NS2PM).

XX

KW Dengue haemorrhagic fever; DHF; dengue fever; DF; dengue shock
DSS; DEN1 polypeptides; Dengue Fever Virus Type; amplification
KW polymerase chain reaction; PCR; ss.

XX

OS Synthetic.

XX

PN WO9322440-A1.

XX

PD 11-NOV-1993.

XX

PF 28-APR-1993; 93WO-CA000182.

XX

PR 29-APR-1992; 92GB-00009243.

XX

PA (UYSI-) UNIV SINGAPORE NAT.

XX

PI Tan Y, Fu J, Tan B, Yap E, Chan Y;

XX

DR WPI; 1993-368739/46.

XX

PT New Dengue virus type 1 strain - used to obtain prods. for det

diagnosis, vaccines and treatment involving virus.

XX

PS Example 2; Page 18; 55pp; English.

XX

CC DEN1 virus, strain S275/90 was isolated from the serum of a de
CC haemorrhagic fever (DHF) patient. RNA was isolated from the vi
CC used to prepare cDNA encoding DEN1 polypeptides. Dengue Virus
CC prods. can be used for detection, diagnosis, vaccines (inactiv
CC or treatment of DEN1 infections. The sequences given in AAQ514
CC oligonucleotides used to prepare cDNA fragments corresp. to de
CC proteins, by PCR. (Updated on 25-MAR-2003 to correct PN field.

XX

SQ Sequence 29 BP; 9 A; 5 C; 9 G; 6 T; 0 U; 0 Other;

Query Match

Best Local Similarity 57.1%; Score 16; DB 2; Length 29;

Matches 19; Conservative 0; Mismatches 5; Indels 0;

QY 1 AGCATCATCTCTGTCAGTGCAGG 24

||||| ||||| ||||| ||||| |||||

Db 2 ATCAGAAATCTCTGCGAGGTGAGG 25

RESULT 12

AAV39800

standard; cDNA; 42 BP.

1 (first entry)

1 tide SEQ ID NO:318 from WO9820166.

ometry; diagnosis; detection; biological sample; infection; disease; chromosomal abnormality; identification; heredity; organism; telomerase activity; oncogene mutation; specific sequence; primer; ss.

12.

3.

1; 97WO-US020444.

1; 96US-00744481.

1; 96US-00744590.

1; 96US-00746036.

1; 96US-00746055.

1; 97US-00786988.

1; 97US-00787639.

1; 97US-00933792.

1; 97US-00947801.

JUENOM INC.

Tang K, Fu D, Siebert CW, Little DP, Higgins GS;

Hammer-Bemar B, Jurinke C, Van Den Boom D, Xiang G;

86975/25.

nucleic acid by mass spectrometric analysis - for detecting ds, telomerase activity, oncogene mutations, or cancer-sequences, for diagnosis of disease.

Page 335; 478pp; English.

has been developed for determining the sequence of a target d. The process comprises: (i) generating at least two F from the target nucleic acid; and (ii) analysing F by mass Y (MS). The sequences in AAV39483 to AAV39592 are specifically mers for use in the mass spectrometric analysis of the above e process is used to detect genetic diseases (e.g. , thalassemia, Duchenne muscular dystrophy, Alzheimer's , stic fibrosis and many others) or chromosomal abnormalities osition); infections and cancers; also for establishing d heredity. Particular applications are diagnosis of ma, detecting telomerase, determining family relationships and bility, and in genetic fingerprinting. Compared with known ng MS, this process requires fewer specific reagents and is ed to automation. Extended primers are shorter; primer s more efficient and the process allows detection of many imultaneously. The present sequence represents an tide from the present invention, which is not actually ithin the specification, only within the sequence listing

1 BP; 12 A; 12 C; 9 G; 8 T; 0 U; 1 Other;

ilarity 57.1%; Score 16; DB 2; Length 42;

Conservative 79.2%; Pred. No. 3e+03;

Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CATCCTCTGCATGGTCAGGTCA 27

||||| ||| ||| ||| ||| |||

CATCAACTGGAGATCAGGTCA 24

RESULT 13

AAV45436/c

ID AAV45436 standard; DNA; 30 BP.

XX

AC AAV45436;

XX

DT 18-JAN-1999 (first entry)

XX

DE Aspergillus oryzae pyrG gene PCR primer hembdel.A.

XX

KW 5-Aminolevulinic acid synthase; hema gene; respiratory deficie

KW

oxidative phosphorylation; PCR; primer; pyrG gene; ss.

XX

OS Synthetic.

OS

XX Aspergillus oryzae.

XX

PN WO9841640-A1.

XX

PD 24-SEP-1998.

XX

PF 17-MAR-1998; 98WO-US005156.

XX

PR 17-MAR-1997; 97US-00819458.

XX

PA (NOVO) NOVO-NORDISK AS.

PA

(NOVO) NOVO NORDISK BIOTECH INC.

XX

PI Jensen EB, Cherry JR, Elrod SL;

XX

WPI; 1998-521226/44.

XX

Production of polypeptide in respiratory-deficient cells trans; construct - that complements the defect and encodes polypeptid

PT

production of defective cells by disrupting gene essential for

PT

phosphorylation.

XX

Example 9; Page 33; 57pp; English.

XX

Primer hembdel.A and primer hembdel.A (see AAV45435) were used amplification of a 4.1 kb fragment of the Aspergillus oryzae p containing both 5' and 3' flanking DNA, including direct repea to facilitate recombination and removal of a pyrG marker. The l

CC

was used in the construction of a hemaDelta::pyrG allele (see)

CC

The invention relates to methods for producing polypeptides in

CC

respiratory-deficient cells (e.g. haem-deficient cells). It in

CC

transforming a respiratory-deficient cell with a first nucleic

CC

sequence (e.g. hema gene) which complements the respiratory def

CC

with a second nucleic acid sequence that encodes the respiratory del

CC

culturing the cell, and isolating the polypeptide from the med

CC

method of producing a respiratory-deficient cell, e.g. by disr

CC

gene in a haem-deficient mutant cell, is also claimed

XX

Sequence 30 BP; 10 A; 4 C; 12 G; 4 T; 0 U; 0 Other;

SQ

Query Match 55.7%; Score 15.6; DB 2; Length 30;

Best Local Similarity 81.8%; Pred. No. 4.2e+03;

Matches 18; Conservative 0; Mismatches 4; Indels 0;

QY 1 AGCATCATCCTCTGCATGGTCA 22

||||| ||| ||| ||| ||| |||

DB 26 ATCGTCATCCTCTGCCTTCGTCA 5

RESULT 14

ABN39943

ID ABN39943 standard; DNA; 60 BP.

XX

AC ABN39943;

XX

DT 15-JUL-2002 (first entry)

XX

DE Human spliced transcript detection oligonucleotide SEQ ID NO:12

Human; mouse; rat; splice transcript; detection; RNA transcript
splice variant; transcriptome; oligonucleotide library; ss.

ns.

9-A2.

2.

1; 2001WO-IB001903.

0; 2000US-0221607P.

1; 2001US-0287724P.

MPUGEN INC.

Wasserman A, Mintz E, Mintz L, Faigler S;

257383/30.

oligonucleotide libraries comprising oligonucleotides which
selectively hybridize to mRNAs transcribed from a transcriptio
genome, useful for detecting tissue-, pathology-, and developm
specific genes.

SEQ ID NO 12691; 47pp; English.

The present invention describes oligonucleotide libraries for
messenger RNAs that populate a (sub-)transcriptome, where the
(sub-)transcriptome comprises messenger RNAs transcribed from multi
transcription units that populate a genome. The library compris
oligonucleotides, each capable of hybridising selectively to a
messenger RNAs transcribed from a given transcription unit of
which encodes one or more messenger RNA splice variants. The
oligonucleotide libraries are useful for detecting mRNAs from
biological sample, in expression profiling studies, in qualita
tively characterising the corresponding transcriptome, and in
detecting RNA transcripts and splice variants of human or anim
transcriptomes. The libraries may also be used as specialised
libraries to detect transcripts of a sub-transcriptome under a
biological or pathological state, and so allowing the detectio
of pathology-specific genes such as those genes only expres
sion under a specific pathological condition; to detect
specific genes; and to detect RNA transcripts and splice
variants of a transcriptome of a patient suffering from a part
of a disorder. ABN27253 to ABN59589 represent oligonucleotide sequ
ences, humans and mice, which are used in the exemplification o
present invention. N.B. The sequence data for this patent did
part of the printed specification, but was obtained in electro
directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

0 BP; 14 A; 18 C; 16 G; 12 T; 0 U; 0 Other;

Query Match 55.0%; Score 15.4; DB 6; Length 60;

Best Local Similarity 76.0%; Pred.No. 5.8e+03;

Conservative 0; Mismatches 6; Indels 0; Gaps 0;

ATCATCCTCTGATGTCAGGTCA 27

|||||

ATGGGCCTCTACATCTCAGGACA 60

standard; DNA; 60 BP.

2 (first entry)

Angiogenesis-inhibiting protein receptor coding sequence SEQ I

Human; mouse; rat; splice transcript; detection; RNA transcript
splice variant; transcriptome; oligonucleotide library; ss.
Homo sapiens.

WO200210449-A2.

07-FEB-2002.

20-JUL-2001; 2001WO-IB001903.

28-JUL-2000; 2000US-0221607P.

02-MAY-2001; 2001US-0287724P.

(COMP-) COMPUGEN INC.

Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

WPI; 2002-257383/30.

New oligonucleotide libraries comprising oligonucleotides whic
selectively hybridize to mRNAs transcribed from a transcriptio
genome, useful for detecting tissue-, pathology-, and developm
specific genes.

Example 1; SEQ ID NO 9909; 47pp; English.

The present invention describes oligonucleotide libraries for
messenger RNAs that populate a (sub-)transcriptome, where the
(sub-)transcriptome comprises messenger RNAs transcribed from multi
transcription units that populate a genome. The library compris
oligonucleotides, each capable of hybridising selectively to a
messenger RNAs transcribed from a given transcription unit of
which encodes one or more messenger RNA splice variants. The
oligonucleotide libraries are useful for detecting mRNAs from
biological sample, in expression profiling studies, in qualita
tively characterising the corresponding transcriptome, and in
detecting RNA transcripts and splice variants of human or anim
transcriptomes. The libraries may also be used as specialised
libraries to detect transcripts of a sub-transcriptome under a
biological or pathological state, and so allowing the detectio
of pathology-specific genes such as those genes only expres
sion under a specific pathological condition; to detect
specific genes; and to detect RNA transcripts and splice
variants of a transcriptome of a patient suffering from a part
of a disorder. ABN27253 to ABN59589 represent oligonucleotide sequ
ences, humans and mice, which are used in the exemplification o
present invention. N.B. The sequence data for this patent did
part of the printed specification, but was obtained in electro
directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 60 BP; 16 A; 14 C; 17 G; 13 T; 0 U; 0 Other;

Query Match 55.0%; Score 15.4; DB 6; Length 60;

Best Local Similarity 94.1%; Pred.No. 5.8e+03;

Matches 16; Conservative 0; Mismatches 1; Indels 0;

9 CCTCTGATGTCAGGT 25

|||||

49 CCTCTGATGTCAGGT 33

RESULT 16

AAA68232

ID AAA68232 standard; DNA; 33 BP.

XX AAA68232;

AC AAA68232;

XX 27-OCT-2000 (first entry)

XX Angiogenesis-inhibiting protein receptor coding sequence SEQ I

XX Angiogenesis-inhibiting protein receptor; angiogenesis; angios

plasma; laminin; treatment; wound healing; solid tumour; scleroderma; myocardial angiogenesis; Crohn's disease; bilateral; arteriovenous malformation; rubeosis; cancer; tinopathy; arthritis; wound healing; peptic ulcer; r related disease; fracture; cat scratch fever; ds.

-A2.

; 99WO-US028897.

; 98US-00206059.

REMED INC.

J, Sim Kl;

12290/35.

nesis-inhibiting protein receptors, useful in methods for seases and processes that are mediated by angiogenesis, such as psoriasis, scleroderma and myocardial angiogenesis.

ge 96; 10pp; English.

ion relates to angiogenesis-inhibiting protein receptors, and uences encoding them. Angiogenesis is the generation of new ls into a tissue, and normally occurs in wound healing, foetal al development and the formation of the corpus luteum, and placenta. Angiostatin is a protein (see AAB16450 and involved in angiogenesis, and has an amino acid sequence that of a plasminogen fragment (see murine plasminogen Angiostatin has the ability to inhibit angiogenesis. is also an angiogenesis inhibiting protein (see AAB16451 and Sequences AAB68242 and AAB16522 represent coding and protein f human laminin. Laminin is an angiostatin binding protein, the peptides of the invention share homology with regions of ptides AAB16452-B16521 (excluding AAB16490) are the s-inhibiting protein receptor fragments of the invention. The nd either angiostatin or endostatin and can be used in methods g diseases and processes that are mediated by angiogenesis, id tumours, psoriasis, scleroderma, myocardial angiogenesis, ease, cerebral collaterals, arteriovenous malformations, iabetic retinopathy, arthritis, wound healing, peptic ulcers, r related diseases, fractures, placenta and cat scratch are useful for the detection and prognosis of cancer. DNA .628204-A628241 encode the peptides of the invention

BP; 5 A; 10 C; 9 G; 9 T; 0 U; 0 Other;

54.3%; Score 15.2; DB 3; Length 33;

ilarity 85.0%; Pred. No. 6.4e+03;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TCATCATCTGTCATGGT 20

|||||

TCCTCCTCATCTGTCATGGT 24

; standard; DNA; 39 BP.

l (first entry)

; peptide analogue coding sequence SEQ ID NO: 23.

; 5; glutamic acid decarboxylase; type 1 diabetes;

XX insulin dependent diabetes mellitus; IDDM; analogue; ds.
XX Homo sapiens.
XX WO200113934-A1.
XX 01-MAR-2001.
XX 17-AUG-2000; 2000WO-US022661.
XX 23-AUG-1999; 99US-00379211.
XX (VIRG-) VIRGINIA MASON RES CENT.
XX Nepom GT, Masewicz S, Nepom BS;
XX WPI; 2001-226589/23.
XX Novel peptides and peptide analogs designed from human pancreatic
XX beta cell autoantigen GAD65, useful for the treatment and preve
XX type 1 diabetes, pre-diabetes or recurring autoimmunity.

PS Disclosure; Page 53; 57pp; English.

XX The present invention provides a number of peptide analogues of
XX GAD65 protein (the 65 kDa isoform of glutamic acid decarboxylase
XX are useful as they antagonise autoimmune T cell activation in
XX GAD65 and prevent type 1 diabetes (also known as insulin depend
XX diabetes mellitus or IDDM). They can thus be used in the treat
XX diabetes, as well as in the prevention of its occurrence in an
XX with pre-IDDM. The present sequence is an example of a coding s
XX a peptide analogue of the invention.

XX SQ Sequence 39 BP; 10 A; 12 C; 7 G; 10 T; 0 U; 0 Other;

Query Match

Best Local Similarity 54.3%; Score 15.2; DB 5; Length 39;

Matches 17; Conservative 85.0%; Pred. No. 6.6e+03;

Mismatches 0; Indels 0;

OY 8 TCCTCTGTCATGGTCAGGTCA 27

|||||

Db 5 TCTTCCGTCATGGTCATGTCA 24

RESULT 18

AAV20388

ID AAV20388 standard; DNA; 56 BP.

XX AAV20388;

XX 26-JUN-1998 (first entry)

XX Primer 5 for human immunity related factor cDNA.

XX Lymph node; human; immunity related factor; research; treatment

XX immune disease; infectious disease; PCR primer; ss.

XX Synthetic.

OS Homo sapiens.

XX JPL0072495-A.

XX 17-MAR-1998.

XX 11-JUN-1997; 97JP-00153218.

XX 13-JUN-1996; 96JP-00152362.

XX (ASAH) ASAHI KASEI KOGYO KK.

XX WPI; 1998-234766/21.

XX Immunity related factor - useful in the treatment of immune re.
PT

ATCCTTCATGTCAGGT 25
|||||
ATCCACTGCTTGGTCAGGT 37

-andard; DNA; 25 BP.

3 (first entry)

array DNA oligonucleotide SEQ ID NO 9236.

robe; expressed sequence tag; microarray; gene expression;
iation; biallelic marker; polymorphism; human;
ies comparison.

1S.

10-A1.

3.

2; 2002US-00098263.

1; 2001US-0276759P.

FYMETRIX INC.

2;

567953/53.

of nucleic acid probes, useful for in situ hybridization, in
Northern or dot-blot hybridization to identify or detect the
r specific mutations of any gene.

EQ ID NO 9236; 9pp; English.

ion discloses a microarray comprising a plurality of nucleic
s including one of 2,018,500 fully defined sequences, or its
tch, perfect mismatch, antisense match or antisense mismatch.
sed is a method of gene expression analysis. The array is used
ing gene expression levels by hybridisation to a DNA library,
s of genetic variation or in hybridisation of tag-labelled
The nucleic acid probes are specifically designed for analysis
t one target sequence. The method of analysis comprises
g at least one or more nucleic acids to at least two or more
id probes and detecting the hybridisation. The nucleic acid
attached to a solid support. The analysis comprises monitoring
sion levels, identifying biallelic markers or polymorphisms,
members of a gene and a cross-species comparison. Each of the
ids further comprises a tag sequence. The array of nucleic acid
useful in situ hybridisation, in Southern, Northern or dot-
disation to identify or detect the sequence or specific
of any gene, in mapping the 5' termini of mRNA molecules by
ensions or in screening cDNA or genomic libraries or subclones
onal subclones containing segments of DNA that have been
nd previously sequenced. The sequence presented is one of the
id probes incorporated in the microarray. Note: The sequence
his patent can also be obtained in electronic format directly
at seqdata.uspro.goc/sequence.html

5 BP; 4 A; 7 C; 6 G; 8 T; 0 U; 0 Other;

53.6%; Score 15; DB 8; Length 25;
milarity 78.3%; Pred. No. 7.4e+03;
Conservative 0; Mismatches 5; Indels 0; Gaps 0;

ATCCTTCATGTCAGGT 28

Db 3 CGTCTCTTCATGTCAGGCAT 25

RESULT 22

AAF8886/c

ID AAF8886 standard; DNA; 41 BP.

XX

AC AAF8886;

XX

DT 07-JAN-2003 (first entry)

XX

DE Aldehyde/ketone reductase 8.8 probe SEQ ID 9.

XX

KW Aldehyde/ketone reductase 8.8; malignant tumour; haemopathy;
KW human immunodeficiency virus; HIV infection; immunological dis
KW inflammation; probe; detection; ss.

XX

OS Unidentified.

XX

PN CN1352260-A.

XX

PD 05-JUN-2002.

XX

PF 10-NOV-2000; 2000CN-00127325.

XX

PR 10-NOV-2000; 2000CN-00127325.

XX

PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX

PI Mao Y, Xie Y;

XX

DR WPI; 2002-714449/78.

XX

PT New polypeptide-aldehyde/ketone reductase 8.8 and polynucleoti
PT encoding such polypeptide.

XX

PS Example 6; Page 19 (Disclosure); 32pp; Chinese.

XX

CC This invention describes a novel aldehyde/ketone reductase, 8.
CC polynucleotides for encoding this polypeptide and a DNA recomb
CC process to produce the polypeptide. The invention also disclos
CC the polypeptide in treating various diseases, such as malignan
CC haemopathy, human immunodeficiency virus (HIV) infection, immu
CC diseases and various inflammations. This sequence represents a
CC in the detection of the aldehyde/ketone reductase 8.8 describe
CC disclosure of the invention

XX

SQ Sequence 41 BP; 7 A; 9 C; 16 G; 9 T; 0 U; 0 Other;

Query Match 53.6%; Score 15; DB 6; Length 41;

Best Local Similarity 78.3%; Pred. No. 8.1e+03;

Matches 18; Conservative 0; Mismatches 5; Indels 0;

QY 3 CATCATCCTCTGCATGTCAGGT 25

Db 29 CCTCAACCTGGCATGTCAGGT 7

RESULT 23

AAH43442

ID AAH43442 standard; DNA; 44 BP.

XX

AC AAH43442;

XX

DT 04-DEC-2001 (first entry)

XX

DE Primer J 903 p7H6.

XX

KW Polymerase chain reaction; primer; amplify; PCR; hepatitis C v
KW NS2/3 protease; homodimer; autoprolytic activity; inhibit;

XX

OS Synthetic.

I-A2.

2001WO-IB000527.
2000GB-00006537.

RICERCHER BIOL MOLECOLARE ANGELETTI.

C. Pallaro M, Lahm A;

390054/66.

is C virus (HCV) NS2/3 protease fragment having
lytic activity when present as homodimer, useful for
modulators of HCV NS2/3 protease that are useful for treating
ion.

Page 43; 80pp; English.

ses given in AH43431-46 are primers which were used to amplify
fragments of hepatitis C virus (HCV) NS2/3 protease. The
cDNA's encode fragments which have as the N-terminal, an amino
is at position 903-913 in HCV NS2/3 protease precursor and as
inal an amino acid that is at position 1206-1657 in HCV NS2/3
recursor. The protein fragments, in homodimeric form, have
lytic activity. They are useful for testing the ability of an
modulate activity of HCV NS2/3 protease which involves bringing
nt into contact with the protein fragment or a homodimer and
g formation of the homodimer and/or HCV NS2/3 protease
The modulator compounds identified using this method modulate,
inhibit, the autoproteolytic activity of NS2/3 precursor and
are useful for treating HCV infection or for manufacturing a
n, medicament or drug for treating HCV infection

4 BP; 11 A; 12 C; 10 G; 11 T; 0 U; 0 Other;

53.6%; Score 15; DB 4; Length 44;

milarity 78.3%; Pred. No. 8.2e+03;

Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CATCATCTCTGCATGTCAGG 24
|||||
CATCATCATCATCATCATCAGG 24

standard; DNA; 60 BP.

12 (first entry)

ced transcript detection oligonucleotide SEQ ID NO:31738.

use; rat; splice transcript; detection; RNA transcript;
iant; transcriptome; oligonucleotide library; ss.

ans.

19-A2.

32.

31; 2001WO-IB001903.

30; 2000US-0221607P.

31; 2001US-0287724P.

OMPUGEN INC.

XX Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX WPI; 2002-257383/30.
XX
XX New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription
PT genome, useful for detecting tissue-, pathology-, and developm
PT specific genes.

XX Example 1; SEQ ID NO 31738; 47pp; English.

XX The present invention describes oligonucleotide libraries for
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC transcriptome comprises messenger RNAs transcribed from multi
CC transcription units that populate a genome. The library compri
CC oligonucleotides, each capable of hybridising selectively to a
CC messenger RNAs transcribed from a given transcription unit of
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from
CC biological sample, in expression profiling studies, in qualita
CC quantitatively characterising the corresponding transcriptome,
CC detecting RNA transcripts and splice variants of human or anim
CC transcriptomes. The libraries may also be used as specialised
CC libraries to detect transcripts of a sub-transcriptome under a
CC biological or pathological state, and so allowing the detectio
CC - and pathology-specific genes such as those genes only expres
CC specific tissue under a specific pathological condition; to de
CC developmental specific genes; and to detect RNA transcripts an
CC variants of a transcriptome of a patient suffering from a part
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequ
CC rats, humans and mice, which are used in the exemplification o
CC present invention. N.B. The sequence data for this patent did
CC part of the printed specification, but was obtained in electro
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 60 BP; 13 A; 15 C; 17 G; 15 T; 0 U; 0 Other;

Query Match 53.6%; Score 15; DB 6; Length 60;

Best Local Similarity 78.3%; Pred. No. 8.6e+03;

Matches 18; Conservative 0; Mismatches 5; Indels 0;

QY 2 GCATCATCTCTGCATGTCAGG 24
|||||
Db 25 GCATCACCATCTTCATGTCAGG 3

RESULT 25

ABN59110/c

ID ABN59110 standard; DNA; 60 BP.

XX AC ABN59110;

XX 15-JUL-2002 (first entry)

XX Human spliced transcript detection oligonucleotide SEQ ID NO:3

XX Human, mouse; rat; splice transcript; detection; RNA transcrip
KW splice variant; transcriptome; oligonucleotide library; ss.

XX Homo sapiens.

XX WO200210449-A2.

XX 07-FEB-2002.

XX 20-JUL-2001; 2001WO-IB001903.

XX 28-JUL-2000; 2000US-0221607P.

XX 02-MAY-2001; 2001US-0287724P.

XX (COMP-) COMPUGEN INC.

XX

Wasserman A, Mintz E, Mintz L, Faigler S;

57383/30.

cleotide libraries comprising oligonucleotides which hybridize to mRNAs transcribed from a transcription unit of a full for detecting tissue-, pathology-, and developmental-nes.

SEQ ID NO 31858; 47pp; English.

invention describes oligonucleotide libraries for detecting mRNAs that populate a (sub-)transcriptome, where the (sub-)ome comprises messenger RNAs transcribed from multiple on units that populate a genome. The library comprises several itides, each capable of hybridizing selectively to a set of mRNAs transcribed from a given transcription unit of the genome, ies one or more messenger RNA splice variants. The ide libraries are useful for detecting mRNAs from a sample, in expression profiling studies, in qualitatively or rely characterizing the corresponding transcriptome, and in RNA transcripts and splice variants of human or animal mes. The libraries may also be used as specialized mini o detect transcripts of a sub-transcriptome under a particular or pathological state, and so allowing the detection of tissue ology-specific genes such as those genes only expressed in issue under a specific pathological condition; to detect al specific genes; and to detect RNA transcripts and splice a transcriptome of a patient suffering from a particular BN27253 to ABN59589 represent oligonucleotide sequences from s and mice, which are used in the exemplification of the ention. N.B. The sequence data for this patent did not form a printed specification, but was obtained in electronic format om WIPO at ftp.wipo.int/pub/published_pct_sequences

) BP; 13 A; 15 C; 17 G; 15 T; 0 U; 0 Other;

ilarity 53.6%; Score 15; DB 6; Length 60;

Conservative 78.3%; Pred. No. 8.6e+03; Mismatches 5; Indels 0; Gaps 0;

TATCATCTCTGCATGTCAGG 24

||||| ||||| ||||| ||||| |||||

TATCACCATCTTCATGTTGAGG 3

tandard; DNA; 25 BP.

3 (first entry)

array DNA oligonucleotide SEQ ID NO 19509.

robe; expressed sequence tag; microarray; gene expression; riation; biallelic marker; polymorphism; human; ies comparison.

ns.

10-A1.

3.

2; 2002US-00098263.

1; 2001US-0276759P.

FYMETRIX INC.

IP;

XX
DR

WPI; 2003-567953/53.

New array of nucleic acid probes, useful for in situ hybridizat Southern, Northern or dot-blot hybridization to identify or del sequence or specific mutations of any gene.

Claim 1; SEQ ID NO 19509; 9pp; English.

The invention discloses a microarray comprising a plurality of acid probes including one of 2,018,500 fully defined sequences. perfect match, perfect mismatch, antisense match or antisense Also disclosed is a method of gene expression analysis. The ar in monitoring gene expression levels by hybridisation to a DNA in analysis of genetic variation or in hybridisation of tag-lal compounds. The nucleic acid probes are specifically designed f of at least one target sequence. The method of analysis compri hybridising at least one or more nucleic acids to at least two nucleic acid probes and detecting the hybridisation. The nucle probes are attached to a solid support. The analysis comprises Gene expression levels, identifying biallelic markers or polym or family members of a gene and a cross-species comparison. Ea nucleic acids further comprises a tag sequence. The array of n probes is useful in situ hybridisation, in Southern, Northern blot hybridisation to identify or detect the sequence or speci mutations of any gene, in mapping the 5' termini of mRNA molec primer extensions or in screening cDNA or genomic libraries or for additional subclones containing segments of DNA that have isolated and previously sequenced. The sequence presented is nucleic acid probes incorporated in the microarray. Note: The data from this patent can also be obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html

Sequence 25 BP; 6 A; 7 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 52.9%; Score 14.8; DB 8; Length 25;

Best Local Similarity 88.9%; Pred. No. 9e+03;

Matches 16; Conservative 0; Mismatches 2; Indels 0;

QY 9 CCTCTGCATGTCAGGTC 26

||||| ||||| ||||| |||||

Db 25 CCTCTGGATGTCAGGTC 8

RESULT 27

AAA79182/c

ID AAA79182 standard; DNA; 31 BP.

XX AAA79182;

XX 20-NOV-2000 (first entry)

Human genomic DNA polymorphic site sequence tag SEQ ID NO:552.

Human; genomic DNA; polymorphism; genome; allele-specific; pri hybridisation; polymorphic site; forensic; paternity testing; phenotypic trait; genetic analysis; genetic mapping; ds.

OS Homo sapiens.

XX EF1024200-A2.

XX 02-AUG-2000.

XX 26-JAN-2000; 2000EP-00250023.

XX 27-JAN-1999; 99US-00238402.

XX (AFFY-) AFFYMETRIX INC.

XX Patil N, Shah N, Warrington JA;

XX WPI; 2000-500198/45.

DR

ic polymorphic nucleic acid segments, allele specific primers and methods of analysis, useful for e.g. forensics, paternity genetic mapping,.

age 20; 141pp; English.

: invention describes a nucleic acid segment of 10-100 bases chosen from one of 632 fragments (AAA78631 to AAA79262), segment comprises a polymorphic site or an immediately adjacent complement of the segment. Also described are: (1) an allele oligonucleotide that hybridises to a segment of the novelty; related nucleic acid comprising a sequence of the novelty where phic site within the sequence is occupied by a base other than ace base indicated in the specification; and (3) analysing a id, comprising obtaining a nucleic acid from an individual, and y a base occupying any one of the polymorphic sites of the he nucleic acid segments and method can be used to analyse an s nucleic acid sequences for the presence of polymorphisms. The also be used to test for a disease phenotype and correlate the f the phenotype with a particular polymorphism. The presence of 2 sites are useful for, e.g. forensics, paternity testing, a of polymorphisms with phenotypic traits and for genetic phenotypic traits. AAA78631 to AAA79262 represent sequence nan genomic DNA fragments containing polymorphic sites. The ying the polymorphic site is indicated using IUPAC-IUB re

1 BP; 8 A; 9 C; 9 G; 4 T; 0 U; 1 Other;

ilarity 52.9%; Score 14.8; DB 3; Length 31;

Conservative 1; Mismatches 3; Indels 0; Gaps 0;

GCATCATCTCTGCTGATGT 20

|||||
|:|:|:|:|:|:|
GCTCTGCTCTGCTGATGT 3

standard; RNA; 50 BP.

0 (first entry)

embrane-binding RNA molecule #6.

; antitumour; cellular membrane; binding; liposome; SELEX; ss;
: Evolution of Ligands by Exponential enrichment; permeability.

A1.

19.

19; 99WO-US011297.

18; 98US-0086492P.

19; 99US-00315886.

NIV TECHNOLOGY CORP.

1, Yarus M;

-072599/06.

ucleic acids to phospholipid membranes, particularly for
membrane permeability.

; Fig 3; 67pp; English.

XX

CC The invention relates to a method for binding nucleic acids to
CC by combining a composition containing at least one nucleic acid
CC phospholipid membrane preparation and isolating the membrane-b
CC nucleic acid. Isolation of membrane bound nucleic acid is by a
CC Evolution of Ligands by Exponential enrichment (SELEX) method.
CC especially comprises the generation of a 95 bp oligonucleotide
CC randomised central 50 bp flanked by primer binding sites (see
CC 247154). The oligonucleotides are transcribed from an upstream
CC promoter and the resultant RNA is combined with phosphatidylch
CC liposomes to isolate the best binding sequences. The method is
CC used to isolate RNA molecules able to alter the permeability,
CC channel formation, of membranes, e.g. for treatment of ion-cha
CC diseases such as Liddle's syndrome, cystic fibrosis or pulmona
CC also as selective ionophores (potential antibiotics), and to li
CC membranes, e.g. to assess cellular function, to analyze change
CC membrane structure and fluidity, or to differentiate between t
CC cells. The nucleic acids may also be used to target effector m
CC (e.g. toxins, growth factors, cytokines, ribozymes, or targetin
CC such as antibodies) for treatment or diagnosis, e.g. of tumour
CC pathogenic organisms. This sequence represents an example of a
CC binding RNA oligonucleotide

XX SQ Sequence 50 BP; 7 A; 9 C; 14 G; 0 T; 20 U; 0 Other;

Query Match 52.9%; Score 14.8; DB 3; Length 50;

Best Local Similarity 46.2%; Pred. No. 1e+04;

Matches 12; Conservative 7; Mismatches 7; Indels 0;

QY 1 AGCATCATCTCTGCTGATGTCTGATGTC 26

|||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 7 AUCUUAUUCUGUGUGUGUGUGUGAGGUC 32

RESULT 29

ABZ01817

ID ABZ01817 standard; DNA; 50 BP.

XX AC ABZ01817;

XX DT 09-JAN-2003 (first entry)

DE Human leukocyte gene expression profiling probe SEQ ID NO 1808

XX KW T7; leukocyte; gene expression profiling; allograft rejection;
XX KW atherosclerosis; congestive heart failure; systemic lupus eryt
XX KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infecti
XX KW ss.

XX OS Homo sapiens.

XX PN WO200257414-A2.

XX PD 25-JUL-2002.

XX PF 22-OCT-2001; 2001WO-US047856.

XX PR 20-OCT-2000; 2000US-0241994P.

XX PR 08-JUN-2001; 2001US-0296764P.

XX PA (BTCC-) BIOCARDIA INC.

XX PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phil
XX PI Ly N, Woodward R, Quertemous T, Johnson F;

XX DR WPI; 2002-635525/68.

XX PT New system for leukocyte expression profiling, diagnosing a di
XX PT monitoring (the rate of) progression of a disease, e.g. ather
XX PT or congestive heart failure, comprises diagnostic oligonucleot
XX PS Claim 1; Page 383; Opp; English.

XX

o AAY179867 represent isolated human polymorphic polynucleotide (I), which contain single nucleotide polymorphisms (SNPs). o AAM53329 represent peptides related to human polymorphic peptide sequences. The sequences can be used in gene and protein and in vaccine production. (I) and the polypeptides encoded by e used in the prevention, diagnosis and treatment of diseases with inappropriate expression of polymorphic polypeptides. For (I) may be used to treat disorders by rectifying mutations or in a patient's genome that affect the activity of polypeptides of inactive proteins or to supplement the patients own of polypeptide. Additionally, (I) and its complementary may also be used as DNA probes in diagnostic assays to detect the presence of similar nucleic acids in samples, and

which a proliferation-required gene or its gene product lies on which the test compound that inhibits proliferation of an act; (9) manufacturing an antibiotic; (10) profiling a activity; (11) a culture comprising strains in which the gene overexpressed or underexpressed; (12) determining the extent of the strains is present in a culture or collection of a r (13) identifying the target of a compound that inhibits the ion of an organism. The antisense nucleic acids are useful for g proteins or screening for homologous nucleic acids required ar proliferation to isolate candidate molecules for rational very programs, or for screening homologous nucleic acids or proliferation in cells other than *S. aureus*, *S. typhimurium*, iae or *P. aeruginosa*. The present sequence is one of the 6213 sequences of the invention. Note: The sequence data for this not form part of the printed specification, but was obtained nic format directly from WIPO at nt/pub/published_pct_sequences. (Updated on 27-OCT-2003 to e OS field)

3 BP; 7 A; 13 C; 12 G; 21 T; 0 U; 0 Other;

52.9%; Score 14.8; DB 7; Length 53;

milarity 73.1%; Pred. No. 1e+04; 7; Indels 0; Gaps 0;
Conservative 0; Mismatches 7; Indels 0; Gaps 0;

GCATCATCTCTGTCATGTCAGTTC 26
||||| ||||| ||||| |||||
GCATCAAGCTCAGCAAGTGAAGTC 3

standard; DNA; 60 BP.

12 (first entry)

ced transcript detection oligonucleotide SEQ ID NO:18696.

use; rat; splice transcript; detection; RNA transcript;
lant; transcriptome; oligonucleotide library; ss.

ms.

19-A2.

12.

11; 2001WO-IB001903.

10; 2000US-0221607P.

11; 2001US-0287724P.

OMPUGEN INC.

, Wasserman A, Mintz E, Mintz L, Faigler S;

-257383/30.

nucleotide libraries comprising oligonucleotides which ly hybridize to mRNAs transcribed from a transcription unit of a useful for detecting tissue-, pathology-, and developmental- genes.

; SEQ ID NO 18696; 47pp; English.

nt invention describes oligonucleotide libraries for detecting RNAs that populate a (sub-)transcriptome, where the (sub-)ptome comprises messenger RNAs transcribed from multiple tion units that populate a genome. The library comprises several eotides, each capable of hybridising selectively to a set of RNAs transcribed from a given transcription unit of the genome,

CC which encodes one or more messenger RNA splice variants. The CC oligonucleotide libraries are useful for detecting mRNAs from CC biological sample, in expression profiling studies, in qualita CC quantitatively characterising the corresponding transcriptome, CC detecting RNA transcripts and splice variants of human or anim CC transcriptomes. The libraries may also be used as specialised CC libraries to detect transcripts of a sub-transcriptome under a CC biological or pathological state, and so allowing the detecti CC - and pathology-specific genes such as those genes only expres CC specific tissue under a specific pathological condition; to de CC developmental specific genes; and to detect RNA transcripts an CC variants of a transcriptome of a patient suffering from a part CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequ CC rats, humans and mice, which are used in the exemplification c CC present invention. N.B. The sequence data for this patent did CC part of the printed specification, but was obtained in electr CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences CC
SQ Sequence 60 BP; 16 A; 21 C; 9 G; 14 T; 0 U; 0 Other;

Query Match 52.9%; Score 14.8; DB 6; Length 60;

Best Local Similarity 73.1%; Pred. No. 1.1e+04;

Matches 19; Conservative 0; Mismatches 7; Indels 0;

Qy 3 CATCATCTCTGTCATGTCAGTTCAT 28

Db 2 CTTCACTCCATCCATGCTCAGCAGT 27
||| ||| ||| ||| ||| ||| ||| |||

RESULT 33

ABN43493/C

ID ABN43493 standard; DNA; 60 BP.

XX AC ABN43493;

XX DT 15-JUL-2002 (first entry)

XX DE Human spliced transcript detection oligonucleotide SEQ ID NO:1

XX KW Human; mouse; rat; splice transcript; detection; RNA transcrip

XX KW splice variant; transcriptome; oligonucleotide library; ss.

XX OS Homo sapiens.

XX FN WO200210449-A2.

XX PD 07-FEB-2002.

XX PF 20-JUL-2001; 2001WO-IB001903.

XX PR 28-JUL-2000; 2000US-0221607P.

XX PR 02-MAY-2001; 2001US-0287724P.

XX PA (COMP-) COMPUTGEN INC.

XX PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;

XX DR WPI; 2002-257383/30.

XX PT New oligonucleotide libraries comprising oligonucleotides whi
PT selectively hybridize to mRNAs transcribed from a transcripti
PT genome, useful for detecting tissue-, pathology-, and develop
PT specific genes.

XX PS Example 1; SEQ ID NO 16241; 47pp; English.

XX CC The present invention describes oligonucleotide libraries for
CC messenger RNAs that populate a (sub-)transcriptome, where the
CC)transcriptome comprises messenger RNAs transcribed from mult
CC transcription units that populate a genome. The library compr
CC oligonucleotides, each capable of hybridising selectively to
CC messenger RNAs transcribed from a given transcription unit of
CC which encodes one or more messenger RNA splice variants. The

otide libraries are useful for detecting mRNAs from a sample, in expression profiling studies, in qualitatively or vely characterizing the corresponding transcriptome, and in RNA transcripts and splice variants of human or animal omes. The libraries may also be used as specialised mini to detect transcripts of a sub-transcriptome under a particular or pathological state, and so allowing the detection of tissue ology-specific genes such as those genes only expressed in issue under a specific pathological condition; to detect tal specific genes; and to detect RNA transcripts and splice ABN27253 to ABN59589 represent oligonucleotide sequences from ns and mice, which are used in the exemplification of the vention. N.B. The sequence data for this patent did not form e printed specification, but was obtained in electronic format rom WIPO at ftp.wipo.int/pub/published_pct_sequences

0 BP; 19 A; 16 C; 10 G; 15 T; 0 U; 0 Other;

milarity 52.9%; Score 14.8; DB 6; Length 60;

Conservative 0; Mismatches 7; Indels 0; Gaps 0;

CATCATCTCTGCATGTCAGTCA 27

||||| ||||| ||||| ||||| |||||
CATCATCACTGATAGGATTCA 20

standard; DNA; 22 BP.

3 (first entry)

DNA PCR primer #13.

X; inflammatory disorder; demyelination disease; stroke; rder; infection; cardiomyopathy; atherosclerosis; ache; on; pancreatitis; Von Hippel-Lindau; endometriosis; fertility; a; cirrhosis; inflammatory bowel disease; Crohn's disease; a; autoimmune disease; allergy; AIDS; us host disease; Alzheimer's disease; arthritis; pain; s disease; Huntington's disease; obesity; diabetes; h; hair loss; asthma; schizophrenia; glomerulonephritis; hematosus; psoriasis; antidiabetic; anorectic; metabolic; neuroprotective; cytostatic; antibacterial; virucide; de; antiarteriosclerotic; hypotensive; cerebroprotective; matory; gynaecological; antiinfertility; dermatological; ic; haemostatic; immunosuppressive; antiallergic; tic; anticonvulsant; antieborrheic; antiasthmatic; c; anti-HIV; analgesic; nephrotropic; antipsoriatic; PCR;

ns.

7-A2.

2.

12; 2002WO-US022049.

11; 2001US-0268221P.

11; 2001US-0268496P.

11; 2001US-0268646P.

11; 2001US-0268652P.

11; 2001US-0289136P.

11; 2001US-0289310P.

11; 2001US-0269530P.

11; 2001US-0276405P.

11; 2001US-0276399P.

11; 2001US-0276703P.

PR 23-MAR-2001; 2001US-0278199P.
PR 28-MAR-2001; 2001US-0279274P.
PR 30-MAR-2001; 2001US-0280238P.
PR 02-APR-2001; 2001US-0280899P.
PR 08-AUG-2001; 2001US-0310797P.
PR 14-AUG-2001; 2001US-0312284P.
PR 14-SEP-2001; 2001US-0322294P.
PR 14-SEP-2001; 2001US-0322295P.
PR 18-OCT-2001; 2001US-0330293P.
PR 31-OCT-2001; 2001US-0335104P.
PR 31-OCT-2001; 2001US-0335109P.
PR 21-NOV-2001; 2001US-0332127P.
PR 28-NOV-2001; 2001US-0331772P.
XX
XX (CURA-) CURAGEN CORP.
PA
XX
XX

Guo X, Fernandes E, Li L, Kekuda R, Liu Y, Leite M, Spyt Ji W, Casman SJ, Boldog FL, Patturajan M, Vernet CAM, Bal Malyanekar UM, Tchernev VT, Blalock AD, Gusev VY, Rastelli Mezes PD, Ellerman K, Heyes M, Herrmann JL, Shinkets RA, Pena CEA, Shenoy SG, Taupier RJ, Gerlach V, Gorman L; WPI; 2003-148650/14.

Novel NOVX polypeptide useful for identifying an agent that b; polypeptide, and for treating cardiomyopathy, atherosclerosis, hypertension, infertility, scleroderma, cirrhosis, and inflam disease.

Example 3; Page 415; 566pp; English.

The present invention relates to the isolation of novel human polypeptides referred to as NOVX (NOVI-NOV37), variants of the proteins, and the polynucleotide sequences encoding them. The proteins of the invention share homology to various types of p families such as zinc finger-like proteins, enzymes, receptors lipoproteins. The sequences of the invention may be useful in manufacture of a medicament for treating a syndrome associated human disease. For example they can be used to treat inflam disorders, demyelination disease, renal disorders, infections, cardiomyopathy, atherosclerosis, hypertension, stroke, pancre Hippe-Lindau, endometriosis, fertility, scleroderma, cirrhos inflammatory bowel disease, Crohn's disease, haemophilia, aut diseases, allergies, graft versus host disease, Alzheimer's di arthritis, Parkinson's disease, Huntington's disease, obesity, acne, hair growth/loss, asthma, schizophrenia, AIDS, pain, glomerulonephritis, lupus erythematosus, and psoriasis. The p sequence represents a PCR primer used in the examples of the i invention. Note: SEQ ID Nos 113-460 are known sequences used i purposes

Sequence 22 BP; 4 A; 7 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 52.1%; Score 14.6; DB 7; Length 22;

Best Local Similarity 81.0%; Pred. No. 1.1e+04;

Matches 17; Conservative 0; Mismatches 4; Indels 0;

Qy 3 CATCATCTCTGCATGTCAG 23

Db 1 CCTCATCTCTTTCATGTCAG 21
||||| ||||| ||||| ||||| |||||

RESULT 35

ACD20449

ID ACD20449 standard; DNA; 22 BP.

XX

AC ACD20449;

XX

DT 26-AUG-2003 (first entry)

XX

DE Human NOVX DNA PCR primer #15.

XX

XW Human; NOVX; inflammatory disorder; demyelination disease; stu

rd; infection; cardiomyopathy; atherosclerosis; acne;
 on; pancreatitis; Von Hippel-Lindau; endometriosis; fertility;
 a; cirrhosis; inflammatory bowel disease; Crohn's disease;
 a; autoimmune disease; allergy; AIDS;
 us host disease; Alzheimer's disease; arthritis; pain;
 s disease; Huntington's disease; obesity; diabetes;
 h; hair loss; asthma; schizophrenia; glomerulonephritis;
 hematuria; psoriasis; antidiabetic; anorectic; metabolic;
 neuroprotective; cytostatic; antibacterial; virucide;
 de; antiarteriosclerotic; hypotensive; cerebroprotective;
 matory; gynaecological; antinfertility; dermatological;
 ic; haemostatic; immunosuppressive; antiallergic;
 tic; anticonvulsant; antiseborrhoeic; antiasthmatic;
 c; anti-HIV; analgesic; nephroprotective; antipsoriatic; PCR;
 .

ns.

.7-A2.

12.

12; 2002WO-US022049.

11; 2001US-0268221P.
 11; 2001US-0268496P.
 11; 2001US-0268646P.
 11; 2001US-0268665P.
 11; 2001US-0269136P.
 11; 2001US-0269310P.
 11; 2001US-0269530P.
 11; 2001US-0276405P.
 11; 2001US-0276399P.
 11; 2001US-0276703P.
 11; 2001US-0278199P.
 11; 2001US-0279274P.
 11; 2001US-0280238P.
 11; 2001US-0280899P.
 11; 2001US-0310797P.
 11; 2001US-0312284P.
 11; 2001US-0322294P.
 11; 2001US-0322295P.
 11; 2001US-0330293P.
 11; 2001US-0335104P.
 11; 2001US-0335109P.
 11; 2001US-0332127P.
 11; 2001US-0331772P.

IRAGEN CORP.

arnandes E, Li L, Kekuda R, Liu Y, Leite M, Spytek KA;
 man SJ, Boldog FI, Patturajan M, Vernet CAM, Ballinger RA;
 UM, Tcherev VT, Blalock AD, Gusev VY, Rastelli L;
 Ellerman K, Heyes M, Herrmann JL, Shinkets RA, Ioime N;
 Shenoy SG, Taupier RJ, Gerlach V, Gorman L;
 -148650/14.

(polypeptide useful for identifying an agent that binds to the
 le, and for treating cardiomyopathy, atherosclerosis,
 on, infertility, scleroderma, cirrhosis, and inflammatory bowel

: Page 415; 565pp; English.

it invention relates to the isolation of novel human
 es referred to as NOVX (NOV1-NOV37), variants of these
 and the polynucleotide sequences encoding them. The NOVX
 of the invention share homology to various types of protein
 such as zinc finger-like proteins, enzymes, receptors, and
 ins. The sequences of the invention may be useful in the
 re of a medicament for treating a syndrome associated with a
 ase. For example they can be used to treat inflammatory

CC disorders, demyelination disease, renal disorders, infections,
 CC cardiomyopathy, atherosclerosis, hypertension, stroke, pancre
 CC Hippel-Lindau, endometriosis, fertility, scleroderma, cirrhosi
 CC inflammatory bowel disease, Crohn's disease, haemophilia, aut
 CC diseases, allergies, graft versus host disease, Alzheimer's di
 CC arthritis, Farkinson's disease, Huntington's disease, obesity,
 CC acne, hair growth/loss, asthma, schizophrenia, AIDS, pain,
 CC glomerulonephritis, lupus erythematosus, and psoriasis. The p
 CC sequence represents a PCR primer used in the examples of the i
 CC invention. Note: SEQ ID Nos 113-460 are known sequences used i
 CC purposes

XX Sequence 22 BP; 4 A; 7 C; 2 G; 9 T; 0 U; 0 Other;

Query Match 52.1%; Score 14.6; DB 7; Length 22;
 Best Local Similarity 81.0%; Pred. No. 1.1e+04;
 Matches 17; Conservative 0; Mismatches 4; Indels 0;

Qy 3 CATCATCCTCTGCATGCTCAG 23
 Db 1 CCTCATCCTTTTCATGTTTCTAG 21

RESULT 36

AC100102

ID AC100102 standard; DNA; 25 BP.

XX AC100102;

DT 13-OCT-2003 (first entry)

DE Human microarray DNA oligonucleotide SEQ ID NO 93.

XX EST; ss; probe; expressed sequence tag; microarray; gene expre
 KW Genetic variation; biallelic marker; polymorphism; human;
 XX cross-species comparison.

XX Homo sapiens.

XX US2003104410-A1.

PD 05-JUN-2003.

XX 15-MAR-2002; 2002US-00098263.

XX 16-MAR-2001; 2001US-0276759P.

PA (AFFY-) AFFYMETRIX INC.

XX Mittmann MP;

XX WPI; 2003-567953/53.

XX New array of nucleic acid probes, useful for in situ hybridiza
 PT Southern, Northern or dot-blot hybridization to identify or de
 PT sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 93; 9pp; English.

XX The invention discloses a microarray comprising a plurality of
 CC acid probes including one of 2,018,500 fully defined sequences
 CC perfect match, perfect mismatch, antisense match or antisense
 CC Also disclosed is a method of gene expression analysis. The ar
 CC in monitoring gene expression levels by hybridisation to a DN
 CC analysis of genetic variation or in hybridisation of tag-la
 CC compounds. The nucleic acid probes are specifically designed f
 CC of at least one target sequence. The method of analysis compri
 CC hybridising at least one or more nucleic acids to at least two
 CC nucleic acid probes and detecting the hybridisation. The nucle
 CC probes are attached to a solid support. The analysis comprises
 CC gene expression levels, identifying biallelic markers or polyn
 CC or family members of a gene and a cross-species comparison. Ea
 CC nucleic acids further comprises a tag sequence. The array of i

useful in in situ hybridisation, in Southern, Northern or dot-probe hybridisation to identify or detect the sequence or specific regions of any gene, in mapping the 5' termini of mRNA molecules or additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is a nucleic acid probe incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic form at seqdata.uspto.gov/sequence.html

25 BP; 4 A; 9 C; 5 G; 7 T; 0 U; 0 Other;

Query Match 52.1%; Score 14.6; DB 8; Length 25;

Best Local Similarity 81.0%; Pred. No. 1.1e+04;

Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

AGCATCATCTCTGTCATGTC 21

||||| ||||| ||||| ||||| |||||

AGCATCCGCTCTGTCAGGTC 24

standard; DNA; 25 BP.

13 (first entry)

Microarray DNA oligonucleotide SEQ ID NO 94.

probe: expressed sequence tag; microarray; gene expression; hybridization; biallelic marker; polymorphism; human; comparison.

ins.

110-A1.

13.

12; 2002US-00098263.

11; 2001US-0276759P.

MYMETRIX INC.

IP;

567953/53.

of nucleic acid probes, useful for in situ hybridization, in Northern or dot-blot hybridization to identify or detect the or specific mutations of any gene.

SEQ ID NO 94; 9pp; English.

ion discloses a microarray comprising a plurality of nucleic acid probes including one of 2,018,500 fully defined sequences, or its subclones, perfect mismatch, antisense match or antisense mismatch. The array is a method of gene expression analysis. The array is used for gene expression levels by hybridization to a DNA library, or of genetic variation or in hybridization of tag-labelled nucleic acid probes are specifically designed for analysis of one target sequence. The method of analysis comprises hybridization of at least one or more nucleic acids to at least two or more probes and detecting the hybridization. The nucleic acid probes are attached to a solid support. The analysis comprises monitoring expression levels, identifying biallelic markers or polymorphisms, members of a gene and a cross-species comparison. Each of the probes further comprises a tag sequence. The array of nucleic acid probes is useful in situ hybridization, in Southern, Northern or dot-probe hybridization to identify or detect the sequence or specific

CC mutations of any gene, in mapping the 5' termini of mRNA molecules or additional subclones containing segments of DNA that have been isolated and previously sequenced. The sequence presented is a nucleic acid probe incorporated in the microarray. Note: The sequence data for this patent can also be obtained in electronic form at seqdata.uspto.gov/sequence.html

XX Sequence 25 BP; 5 A; 9 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 52.1%; Score 14.6; DB 8; Length 25;

Best Local Similarity 81.0%; Pred. No. 1.1e+04;

Matches 17; Conservative 0; Mismatches 4; Indels 0

QY 1 AGCATCATCTCTGTCATGTC 21

||||| ||||| ||||| ||||| |||||

Db 4 AGCATCCGCTCTGTCAGGTC 24

RESULT 38

AAV46380/c

ID AAV46380 standard; DNA; 30 BP.

XX

AC AAV46380;

XX

DT 20-NOV-1998 (first entry)

XX

DE PCR primer of the invention.

XX

KW Mouse; CXC chemokine receptor; pre-B cell line DW34;

KW CXC chemokine pre-B cell stimulatory factor PBSF/SDF-1; HIV i;

KW screening; inhibitor; AIDS; PCR primer; ss.

XX

OS Synthetic.

XX

PN WO9835035-A1.

XX

PD 13-AUG-1998.

XX

PF 07-FEB-1997; 97WO-JP000299.

XX

PR 07-FEB-1997; 97WO-JP000299.

XX

PA (SHIO) SHIONOGI & CO LTD.

XX

PI Kishimoto T, Nagasawa T, Tachibana K, Iizasa H, Yoshida N,

PI Nakajima T, Yoshie O;

XX

DR WPI; 1998-447232/38.

XX

PT Mouse CXC chemokine receptor binding to PBSF/SDF-1 pre-B cell

PT factor - is useful for screening of potential HIV infection at

XX

PS Example 5; Page 52; 76pp; Japanese.

XX

CC PCR primers AAV46380-81 are used in the course of the invention

CC specification describes a murine CXC chemokine receptor which

CC the mouse CXC chemokine pre-B cell stimulatory factor PBSF/SDF-

CC nucleic acid is isolated from mouse pre-B cell line DW34. The

CC and cells expressing it can be used in the study and mapping of

CC mechanism of HIV infection and in screening of potential inhib

CC HIV infection and the development of AIDS

XX Sequence 30 BP; 6 A; 7 C; 12 G; 5 T; 0 U; 0 Other;

Query Match 52.1%; Score 14.6; DB 2; Length 30;

Best Local Similarity 81.0%; Pred. No. 1.1e+04;

Matches 17; Conservative 0; Mismatches 4; Indels 0;

QY 6 CATCTCTGTCATGTCAGGTC 26

||||| ||||| ||||| ||||| |||||

Db 27 CATCCCTCTGTCAGGTC 7

standard; DNA; 34 BP.

03 (first entry)

r #6 used for generating chimeric Edg5 receptors.
g; receptor; PCR; primer; ss.

ens.

503-A1.

03.

02; 2002WO-US022346.

01; 2001US-00904099.

ERE TEK.

, Munning JN, Spencer JV;

-221718/21.

tic Edg receptor, useful in high-throughput screening assays,
extracellular and transmembrane domains of a first Edg
and a chimeric intracellular domain of a second Edg receptor.

Page 38; 71pp; English.

it invention relates to Edg receptors (ABP59277-ABP59290). The
ors, are useful in a high-throughput screening assay to
compounds that bind to or modulate the activity of the
ie, in calcium mobilisation assays, binding assays, detection of
tion, or in reporter gene techniques. The present sequence is a
; which was used for generating chimeric Edg1 receptors

14 BP; 7 A; 9 C; 10 G; 8 T; 0 U; 0 Other;

Similarity 52.1%; Score 14.6; DB 7; Length 34;

Best Local Similarity 81.0%; Pred. No. 1.2e+04;

Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ATCTCTGCGTGGTCAAGTC 26

|||||
ATCTCTGCGTGGTCAAGTC 14

standard; DNA; 34 BP.

03 (first entry)

#5 used for generating chimeric Edg5 receptors.

i; receptor; PCR; primer; ss.

ns.

03-A1.

3.

2; 2002WO-US022346.

XX
PR 11-JUL-2001; 2001US-00904099.
XX (CERE-) CERETEK.
XX
XX Shankar G, Munning JN, Spencer JV;
PI WPI; 2003-221718/21.
XX
XX
XX New chimeric Edg receptor, useful in high-throughput screenin
PT comprises extracellular and transmembrane domains of a first
PT receptor, and a chimeric intracellular domain of a second Edg
XX
XX Example; Page 38; 71pp; English.
XX
XX The present invention relates to Edg receptors (ABP59277-ABP5
CC Edg receptors, are useful in a high-throughput screening assa
CC identify compounds that bind to or modulate the activity of t
CC polypeptide, in calcium mobilisation assays, binding assays,
CC CAMP formation, or in reporter gene techniques. The present s
CC PCR primer, which was used for generating chimeric Edg1 recep
XX
XX Sequence 34 BP; 8 A; 10 C; 9 G; 7 T; 0 U; 0 Other;

Query Match 52.1%; Score 14.6; DB 7; Length 34;
Best Local Similarity 81.0%; Pred. No. 1.2e+04;
Matches 17; Conservative 0; Mismatches 4; Indels 0

Qy 6 CATCTCTGCGTGGTCAAGTC 26

Db 1 CATCTCTGCGTGGTCAAGTC 21

Search completed: April 12, 2004, 16:42:48
Job time : 208.077 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

ncleic search, using sw model

April 12, 2004, 15:31:02 ; Search time 478.769 Seconds
(without alignments)
2534.843 Million cell updates/sec

US-10-090-326-23

28

1 agcatatccctctgcaggtcaggtcat 28

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

3470272 seqs, 21671516995 residues

: hits satisfying chosen parameters: 1685580

length: 0
length: 60

! Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

GenEmbl.*

1: gb_ba.*
2: gb_htg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rod.*
36: em_htg_mam.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

is the number of results predicted by chance to have a

score greater than or equal to the score of the result being
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Descrip
1	20	71.4	20	6	AX001634	AX00163
2	20	71.4	20	6	AX002137	AX00213
3	20	71.4	20	6	AX816396	AX81639
4	20	71.4	20	6	BD195919	BD19591
5	18	64.3	30	6	A38653	A38653
6	17.2	61.4	40	6	AX538397	AX53839
7	17	60.7	40	6	AX538396	AX53839
8	16	57.1	29	6	A75717	A75717
9	16	57.1	29	6	E06837	E06837
10	16	57.1	42	6	AX328821	AX32882
11	16	57.1	42	6	BD132386	BD13238
12	15.6	55.7	30	6	AR069517	AR06951
13	15.6	55.7	30	6	BD195684	BD19568
14	15.2	54.3	33	6	BD266770	BD26677
15	15.2	54.3	33	6	AX395703	AX39570
16	15.2	54.3	35	6	A11296	A11296
17	15.2	54.3	38	6	A11037	A11037
18	15.2	54.3	41	6	A11295	A11295
19	15.2	54.3	41	6	A11295	A11295
20	15.2	54.3	56	6	E15475	E15475
21	15.2	54.3	58	6	AX327977	AX32797
22	15	53.6	44	6	AX254656	AX25465
23	14.8	52.9	31	6	BD002886	BD00288
24	14.8	52.9	40	6	A83618	A83618
25	14.8	52.9	46	6	AX598134	AX59813
26	14.8	52.9	50	6	AR148167	AR14816
27	14.8	52.9	51	6	AX157925	AX15792
28	14.8	52.9	60	6	BD227015	BD22701
29	14.6	52.1	22	6	AX769362	AX76936
30	14.6	52.1	22	6	AX769365	AX76936
31	14.6	52.1	40	6	AR148762	AR14876
32	14.6	52.1	45	6	AX234368	AX23436
33	14.6	52.1	46	6	AX234359	AX23435
34	14.6	52.1	51	6	AX165131	AX16513
35	14.4	51.4	26	6	AR028646	AR02864
36	14.4	51.4	26	6	AR053739	AR05373
37	14.4	51.4	26	6	AR146239	AR14623
38	14.4	51.4	26	6	AR178189	AR17818
39	14.4	51.4	26	6	I73318	I73318
40	14.4	51.4	26	6	AR214471	AR21447
41	14.4	51.4	26	6	AR274829	AR27482
42	14.4	51.4	31	6	AX248051	AX24805
43	14.4	51.4	42	6	I43112	I43112
44	14.4	51.4	47	6	AR06364	AR06364
45	14.4	51.4	47	6	BD069870	BD06987
46	14.4	51.4	47	6	AR166270	AR16627
47	14.4	51.4	51	6	AR147183	AR14718
48	14.4	51.4	53	6	BD083543	BD08354
49	14.4	51.4	54	6	AX203052	AX20305
50	14.4	51.4	54	6	AR147184	AR14718
51	14.4	51.4	55	6	AX023568	AX02356
52	14.4	51.4	55	6	BD083544	BD08354
53	14.4	51.4	55	6	BD016506	BD01650
54	14.2	50.7	22	6	BD131527	BD13152
55	14.2	50.7	24	6	BD131527	BD13152
56	14.2	50.7	29	6	AR126584	AR12658
57	14.2	50.7	30	6	BD174399	BD17439
58	14.2	50.7	41	6	AX513920	AX51392
59	14.2	50.7	41	6	AX519259	AX51925
60	14.2	50.7	44	6	AX128565	AX12856
61	14.2	50.7	45	6	BD247648	BD24764
62	14.2	50.7	45	6	AR345117	AR34511
63	14.2	50.7	51	6	A45055	A45055
64	14.2	50.7	51	6	AR029671	AR02967
65	14.2	50.7	51	6	AX159509	AX15950

50.7	51	6	AX204361	Sequence	C 139	13.6	48.6	25	6	AX615701	AX615701
50.7	57	6	AX5746	Sequence 3	C 140	13.6	48.6	25	6	AX615702	AX615702
50.7	57	6	AX372860	Sequence	C 141	13.6	48.6	30	6	AX793680	AX793680
50.7	58	12	AY199433	Arabidops	142	13.6	48.6	34	6	AX855288	AX855288
50.0	25	6	AX224545	Sequence	143	13.6	48.6	34	6	117719	117719
50.0	27	6	AX662247	Sequence	144	13.6	48.6	34	6	128967	128967
50.0	29	6	AX099620	Sequence	145	13.6	48.6	34	6	138631	138631
50.0	29	6	BD063996	Secreted	146	13.6	48.6	34	6	138889	138889
50.0	30	6	E27900	Yeast with	147	13.6	48.6	34	6	168974	168974
50.0	30	6	BD016617	Genes and	148	13.6	48.6	36	6	168976	168976
50.0	31	6	AX538109	Sequence	149	13.6	48.6	36	6	AR253572	AR253572
50.0	32	6	BD022557	Multi-fun	150	13.6	48.6	36	6	AR253574	AR253574
50.0	35	6	AR166262	Sequence	151	13.6	48.6	36	6	AX696627	AX696627
50.0	38	6	AR03464	Sequence	152	13.6	48.6	36	6	AX696629	AX696629
50.0	41	6	AX515904	Sequence	153	13.6	48.6	40	6	BD188745	BD188745
50.0	41	6	AX515904	Sequence	154	13.6	48.6	40	6	BD188745	BD188745
50.0	45	12	D64063	Synthetic C	155	13.6	48.6	42	6	BD246948	BD246948
50.0	47	6	AX194785	Sequence	C 156	13.6	48.6	44	6	AR096941	AR096941
50.0	50	6	AX418552	Sequence	C 157	13.6	48.6	45	6	AX695192	AX695192
50.0	51	6	AX026023	Sequence	158	13.6	48.6	45	6	AX5567	AX5567
50.0	51	6	AX161873	Sequence	159	13.6	48.6	49	6	AX7605	AX7605
50.0	51	6	AX161874	Sequence	160	13.6	48.6	49	6	AX019331	AX019331
50.0	51	6	AX165491	Sequence	161	13.6	48.6	49	6	AR9797	AR9797
50.0	60	6	E27896	Yeast with	C 162	13.6	48.6	50	6	AR242325	AR242325
50.0	60	6	E41219	Specific cu	C 163	13.6	48.6	51	6	AX165610	AX165610
49.3	20	6	AR231034	Sequence	C 164	13.6	48.6	57	6	BD138415	BD138415
49.3	21	6	AR028691	Sequence	165	13.6	48.6	60	10	AF432391	AF432391
49.3	21	6	AR086502	Sequence	C 166	13.6	48.6	25	6	E05089	E05089
49.3	27	6	AR143805	Sequence	C 167	13.4	47.9	26	6	AR065340	AR065340
49.3	30	6	AX792455	Sequence	C 168	13.4	47.9	27	6	AR365085	AR365085
49.3	32	6	BD261368	Plants, S	C 169	13.4	47.9	27	6	AR365086	AR365086
49.3	32	6	AR184304	Sequence	170	13.4	47.9	29	6	BD191423	BD191423
49.3	32	6	AR431246	Sequence	171	13.4	47.9	30	6	AX792518	AX792518
49.3	32	6	BD132769	Fatty aci	C 172	13.4	47.9	33	6	AR146987	AR146987
49.3	34	6	BD244058	Determina	C 173	13.4	47.9	41	6	AR109079	AR109079
49.3	42	6	A47188	Sequence 1	C 174	13.4	47.9	41	6	AR200734	AR200734
49.3	42	6	I79600	Sequence 1	C 175	13.4	47.9	41	6	AX515868	AX515868
49.3	43	6	I43892	Sequence 20	C 176	13.4	47.9	41	6	AX521125	AX521125
49.3	46	6	BD244069	Determina	C 177	13.4	47.9	41	6	AX521140	AX521140
49.3	50	6	AX204297	Sequence	178	13.4	47.9	43	6	BD232717	BD232717
49.3	51	6	AR343496	Sequence	C 182	13.4	47.9	45	6	AX023259	AX023259
49.3	52	6	AR021007	Sequence	C 183	13.4	47.9	45	6	A48442	A48442
49.3	52	6	AR043422	Sequence	184	13.4	47.9	46	8	S57736	S57736
49.3	52	6	AR043462	Sequence	C 185	13.4	47.9	51	6	AX115441	AX115441
49.3	52	6	AR062337	Sequence	C 186	13.4	47.9	55	6	AR428091	AR428091
49.3	52	6	AR062377	Sequence	C 187	13.4	47.9	60	6	AX454000	AX454000
49.3	52	6	AR183796	Sequence	C 188	13.4	47.9	60	6	AX454001	AX454001
49.3	52	6	AR183836	Sequence	C 189	13.2	47.1	20	6	AR316159	AR316159
49.3	52	6	AR368179	Sequence	C 190	13.2	47.1	21	6	AR272208	AR272208
49.3	54	6	AR368219	Sequence	C 191	13.2	47.1	21	6	AX097296	AX097296
49.3	54	6	BD271048	Method an	C 192	13.2	47.1	24	6	AR167458	AR167458
49.3	54	6	AR258454	Sequence	C 193	13.2	47.1	24	6	114554	114554
49.3	59	6	AX011479	Sequence	C 194	13.2	47.1	24	6	AX05673	AX05673
49.3	59	6	BD225770	Screening	C 195	13.2	47.1	24	6	AX110200	AX110200
49.3	60	3	TG28SRNAB	Tetraricho	C 196	13.2	47.1	25	6	BD245828	BD245828
49.3	60	6	AX453999	Sequence	C 197	13.2	47.1	25	6	AR181350	AR181350
48.6	20	6	AX505100	Sequence	C 198	13.2	47.1	25	6	AX615695	AX615695
48.6	21	6	AR242920	Sequence	C 199	13.2	47.1	25	6	AX615696	AX615696
48.6	21	6	AR363537	Sequence	200	13.2	47.1	26	6	AR090772	AR090772
48.6	21	6	AX384972	Sequence	201	13.2	47.1	26	6	AR197807	AR197807
48.6	23	6	AR102043	Sequence	202	13.2	47.1	26	6	AR259961	AR259961
48.6	23	6	AR134826	Sequence	203	13.2	47.1	29	6	AR429703	AR429703
48.6	23	6	AX708837	Sequence	204	13.2	47.1	30	6	AR142231	AR142231
48.6	23	6	AX708851	Sequence	205	13.2	47.1	30	6	134492	134492
48.6	24	6	AX020807	Sequence	206	13.2	47.1	30	6	157327	157327
48.6	24	6	AX652073	Sequence	207	13.2	47.1	30	6	173205	173205
48.6	25	6	E40339	DNA marker	208	13.2	47.1	30	6	AX449613	AX449613
48.6	25	6	AX615697	Sequence	209	13.2	47.1	30	6	AX791495	AX791495
48.6	25	6	AX615698	Sequence	210	13.2	47.1	30	6	AX792499	AX792499
48.6	25	6	AX615699	Sequence	211	13.2	47.1	30	6	AX793843	AX793843

45.7	45.7	38	6	BD057965	BD057965 Nucleic a	C 431	12.6	45.0	25	6	E17259	E17259 F
45.7	45.7	41	6	AX517120	AX517120 Sequence	432	12.6	45.0	25	6	E22978	E22978 V
45.7	45.7	41	6	AX519649	AX519649 Sequence	C 433	12.6	45.0	25	6	E22979	E22979 V
45.7	45.7	42	6	A11038	A11038 Nucleotide	434	12.6	45.0	25	6	AR219926	AR219926
45.7	45.7	42	6	A11039	A11039 Nucleotide	C 435	12.6	45.0	25	6	AR219926	AR219926
45.7	45.7	42	6	A11299	A11299 Nucleotide	C 436	12.6	45.0	25	6	AX609254	AX609254
45.7	45.7	42	6	A11300	A11300 Nucleotide	C 437	12.6	45.0	25	6	AX609397	AX609397
45.7	45.7	43	6	AR061569	AR061569 Sequence	C 438	12.6	45.0	25	6	AX609713	AX609713
45.7	45.7	43	6	AR108468	AR108468 Sequence	C 439	12.6	45.0	25	6	AX615703	AX615703
45.7	45.7	43	6	I16425	I16425 Sequence 25	440	12.6	45.0	27	6	AR126153	AR126153
45.7	45.7	43	6	I66911	I66911 Sequence 25	C 441	12.6	45.0	27	6	AX813718	AX813718
45.7	45.7	43	6	I85005	I85005 Sequence 25	442	12.6	45.0	28	6	AX813719	AX813719
45.7	45.7	43	6	AR263429	AR263429 Sequence	443	12.6	45.0	30	6	AX468557	AX468557
45.7	45.7	45	6	A92629	A92629 Sequence 1	444	12.6	45.0	30	6	AX521574	AX521574
45.7	45.7	45	6	AR152959	AR152959 Sequence	445	12.6	45.0	30	6	AX791712	AX791712
45.7	45.7	45	6	BD264361	BD264361 Methods a	446	12.6	45.0	30	6	AX792861	AX792861
45.7	45.7	45	6	AR199548	AR199548 Sequence	447	12.6	45.0	30	6	AX793820	AX793820
45.7	45.7	45	6	AR374700	AR374700 Sequence	448	12.6	45.0	30	9	HUMPLT22	HUMPLT22
45.7	45.7	45	6	AR409335	AR409335 Sequence	C 449	12.6	45.0	31	6	AR195945	AR195945
45.7	45.7	45	6	AR429076	AR429076 Sequence	C 450	12.6	45.0	31	6	AX248399	AX248399
45.7	45.7	45	6	AX239597	AX239597 Sequence	C 451	12.6	45.0	31	6	AX249041	AX249041
45.7	45.7	45	6	BD022692	BD022692 Method fo	452	12.6	45.0	32	6	AR102441	AR102441
45.7	45.7	45	6	BD056462	BD056462 Novel low	453	12.6	45.0	32	6	AR219355	AR219355
45.7	45.7	46	6	BD140557	BD140557 Polypepti	454	12.6	45.0	32	6	BD138423	BD138423
45.7	45.7	46	6	AX800151	AX800151 Sequence	C 455	12.6	45.0	33	6	AR4476	AR4476 S
45.7	45.7	47	6	AR290446	AR290446 Sequence	C 456	12.6	45.0	33	6	AR279934	AR279934
45.7	45.7	47	6	BD080451	BD080451 Methods f	457	12.6	45.0	33	6	AX306751	AX306751
45.7	45.7	51	6	AR077801	AR077801 Sequence	C 458	12.6	45.0	33	6	AX306752	AX306752
45.7	45.7	51	6	BD227170	BD227170 Protease	C 459	12.6	45.0	33	6	AX427375	AX427375
45.7	45.7	51	6	AR368746	AR368746 Sequence	C 460	12.6	45.0	33	6	BD082556	BD082556
45.7	45.7	51	6	AR392701	AR392701 Sequence	C 461	12.6	45.0	34	6	AX548220	AX548220
45.7	45.7	51	6	AX158409	AX158409 Sequence	462	12.6	45.0	35	6	AX794614	AX794614
45.7	45.7	51	6	AX158411	AX158411 Sequence	463	12.6	45.0	35	6	AX794663	AX794663
45.7	45.7	51	6	AX158412	AX158412 Sequence	464	12.6	45.0	36	6	A51534	A51534 S
45.7	45.7	51	6	AX162007	AX162007 Sequence	465	12.6	45.0	36	6	A51562	A51562 S
45.7	45.7	51	6	AX204357	AX204357 Sequence	466	12.6	45.0	36	6	A87816	A87816 S
45.7	45.7	51	9	HSCDICC	X79310 H. sapiens C	467	12.6	45.0	36	6	A91148	A91148 S
45.7	45.7	52	14	ADYLTR	M17114 Avian egg d	468	12.6	45.0	36	6	AR084288	AR084288
45.7	45.7	54	6	I51658	I51658 Sequence 5	469	12.6	45.0	36	6	AR119408	AR119408
45.7	45.7	54	6	AX471970	AX471970 Sequence	470	12.6	45.0	36	6	AR173499	AR173499
45.7	45.7	59	6	AR87307	AR87307 Sequence 32	471	12.6	45.0	36	6	I95566	I95566 S
45.7	45.7	59	6	BD057385	BD057385 Protein c	472	12.6	45.0	36	6	AR206887	AR206887
45.7	45.7	60	6	AR172702	AR172702 Sequence	C 473	12.6	45.0	36	6	AX026033	AX026033
45.7	45.7	60	6	AR178646	AR178646 Sequence	C 474	12.6	45.0	36	6	BD064628	BD064628
45.7	45.7	60	6	BD231090	BD231090 Shuffling	475	12.6	45.0	36	6	BD067141	BD067141
45.7	45.7	60	6	AR181217	AR181217 Sequence	476	12.6	45.0	36	6	BD135011	BD135011
45.7	45.7	60	6	AR199898	AR199898 Sequence	477	12.6	45.0	37	6	AR110221	AR110221
45.7	45.7	60	6	AR231846	AR231846 Sequence	C 478	12.6	45.0	37	6	AR169980	AR169980
45.7	45.7	60	6	AR343321	AR343321 Sequence	C 479	12.6	45.0	37	6	AR171789	AR171789
45.7	45.7	60	6	AR349639	AR349639 Sequence	C 480	12.6	45.0	37	6	AR201269	AR201269
45.7	45.7	60	6	AR391110	AR391110 Sequence	C 481	12.6	45.0	37	6	AR264126	AR264126
45.7	45.7	60	6	AR431553	AR431553 Sequence	C 482	12.6	45.0	37	6	AR264126	AR264126
45.7	45.7	60	6	AX280278	AX280278 Sequence	C 483	12.6	45.0	37	6	AX617004	AX617004
45.7	45.7	60	6	AX280280	AX280280 Sequence	C 484	12.6	45.0	37	6	BD009014	BD009014
45.7	45.7	60	6	BD062835	BD062835 Methods a	C 485	12.6	45.0	37	6	BD189483	BD189483
45.0	45.0	19	6	AX480658	AX480658 Sequence	C 486	12.6	45.0	39	6	AR002625	AR002625
45.0	45.0	20	6	AR118940	AR118940 Sequence	C 487	12.6	45.0	39	6	AR009675	AR009675
45.0	45.0	20	6	I19480	I19480 Sequence 12	C 488	12.6	45.0	40	6	AR205021	AR205021
45.0	45.0	20	6	AX254738	AX254738 Sequence	C 489	12.6	45.0	40	6	AX538569	AX538569
45.0	45.0	20	6	AX255088	AX255088 Sequence	C 490	12.6	45.0	41	6	AR264225	AR264225
45.0	45.0	21	6	BD266110	BD266110 Universal	491	12.6	45.0	41	6	AX514034	AX514034
45.0	45.0	21	6	BD016749	BD016749 Identific	492	12.6	45.0	41	6	AX516099	AX516099
45.0	45.0	22	6	A47330	A47330 Sequence 5	493	12.6	45.0	41	6	AX517505	AX517505
45.0	45.0	22	6	AR097970	AR097970 Sequence	494	12.6	45.0	41	6	AX518475	AX518475
45.0	45.0	22	6	AR145812	AR145812 Sequence	495	12.6	45.0	41	6	AX520503	AX520503
45.0	45.0	22	6	E08175	E08175 Reverse pri	496	12.6	45.0	41	6	AX580276	AX580276
45.0	45.0	22	6	AR283937	AR283937 Sequence	497	12.6	45.0	41	6	AX786441	AX786441
45.0	45.0	22	6	AX356176	AX356176 Sequence	C 498	12.6	45.0	44	6	E43912	E43912 N
45.0	45.0	22	6	AX528227	AX528227 Sequence	C 499	12.6	45.0	45	6	AR099099	AR099099
45.0	45.0	22	6	BD144849	BD144849 A method	C 500	12.6	45.0	45	6	AR199538	AR199538
45.0	45.0	22	6	BD182884	BD182884 PCA3dd3	C 501	12.6	45.0	45	6	AR374690	AR374690
45.0	45.0	24	6	AR098842	AR098842 Sequence	C 502	12.6	45.0	45	6	AR409325	AR409325
45.0	45.0	25	6	E17258	E17258 Primer. 7/1	503	12.6	45.0	45	6	AX224742	AX224742

45.0	45	6	AX239587	Sequence	577	12.4	44.3	31	6	AR259307	AX259307
45.0	45	6	BD056452	Novel low	578	12.4	44.3	31	6	AX172826	AX172826
45.0	46	6	AR277862	Sequence	C 579	12.4	44.3	32	6	AR017664	AR017664
45.0	47	6	AR077831	Sequence	C 580	12.4	44.3	32	6	AR030309	AR030309
45.0	47	6	AR288348	Sequence	C 581	12.4	44.3	32	6	AR042852	AR042852
45.0	48	9	HSTCELL20	X81555 H sapiens r	C 582	12.4	44.3	32	6	AR054846	AR054846
45.0	48	9	S90755	S90755 V delta 1,	C 583	12.4	44.3	32	6	AR058793	AR058793
45.0	48	9	S90756	S90756 V delta 1,	C 584	12.4	44.3	32	6	AR063519	AR063519
45.0	50	6	BD273138	BD273138 Oral immu	C 585	12.4	44.3	32	6	AR064785	AR064785
45.0	51	6	A45564	A45564 Sequence 2	C 586	12.4	44.3	32	6	AR066111	AR066111
45.0	51	6	A45565	A45565 Sequence 3	C 587	12.4	44.3	32	6	AR081343	AR081343
45.0	51	6	AR019328	AR019328 Sequence	C 588	12.4	44.3	32	6	AR092167	AR092167
45.0	51	6	AR069999	AR069999 Sequence	C 589	12.4	44.3	32	6	AR094841	AR094841
45.0	51	6	AR151083	AR151083 Sequence	C 590	12.4	44.3	32	6	AR118158	AR118158
45.0	51	6	I25437	I25437 Sequence 3	C 591	12.4	44.3	32	6	AR122782	AR122782
45.0	51	6	I60623	I60623 Sequence 3	C 592	12.4	44.3	32	6	AR125757	AR125757
45.0	51	6	AR235874	AR235874 Sequence	C 593	12.4	44.3	32	6	AR140767	AR140767
45.0	51	6	AX159328	AX159328 Sequence	C 594	12.4	44.3	32	6	AR140767	AR140767
45.0	51	6	AX164856	AX164856 Sequence	C 595	12.4	44.3	32	6	AR151286	AR151286
45.0	51	6	AX189855	AX189855 Sequence	C 596	12.4	44.3	32	6	AR165500	AR165500
45.0	51	6	AX203981	AX203981 Sequence	C 597	12.4	44.3	32	6	I40674	I40674
45.0	51	6	AX204433	AX204433 Sequence	C 598	12.4	44.3	32	6	I42322	I42322
45.0	51	6	BD073552	BD073552 High expr	C 599	12.4	44.3	32	6	I47169	I47169
45.0	51	10	MUSVHCHM1	BD073552 High expr	C 600	12.4	44.3	32	6	I73549	I73549
45.0	52	6	AR065169	KO0986 Mouse adult	C 601	12.4	44.3	32	6	I93446	I93446
45.0	52	6	I13039	AR065169 Sequence	C 602	12.4	44.3	32	6	I95073	I95073
45.0	54	6	I13040	I13039 Sequence 16	C 603	12.4	44.3	32	6	AR193198	AR193198
45.0	54	6	AX056665	I13040 Sequence 17	C 604	12.4	44.3	32	6	AR221664	AR221664
45.0	54	6	AX912408	AX056665 Sequence	C 605	12.4	44.3	32	6	AR304702	AR304702
45.0	54	6	BD047941	AX912408 Sequence	C 606	12.4	44.3	32	6	AR337318	AR337318
45.0	55	6	E15763	BD047941 Sequence	C 607	12.4	44.3	32	6	AR360441	AR360441
45.0	55	6	E26731	E15763 PCR primer	C 608	12.4	44.3	32	6	AR372166	AR372166
45.0	57	6	AX612611	E26731 Vertebrate	C 609	12.4	44.3	32	6	AX027871	AX027871
45.0	57	6	AX612612	AX612611 Sequence	C 610	12.4	44.3	32	6	AX708231	AX708231
45.0	60	6	AX521516	AX612612 Sequence	C 611	12.4	44.3	32	6	BD022895	BD022895
44.3	17	6	AX730994	AX521516 Sequence	C 612	12.4	44.3	32	6	BD130678	BD130678
44.3	17	6	AX757880	AX730994 Sequence	C 613	12.4	44.3	33	6	AR054771	AR054771
44.3	20	6	BD136731	AX757880 Sequence	C 614	12.4	44.3	33	6	AR066036	AR066036
44.3	22	6	AR136528	BD136731 Sequence	C 615	12.4	44.3	33	6	I08861	I08861
44.3	22	6	AR136593	AR136528 Sequence	C 616	12.4	44.3	33	6	AX172827	AX172827
44.3	23	6	AX675167	AX136593 Sequence	C 617	12.4	44.3	33	6	AX172828	AX172828
44.3	23	6	BD123410	AX675167 Sequence	C 618	12.4	44.3	34	6	AR174599	AR174599
44.3	24	6	AX535397	BD123410 SREP-2 g	C 619	12.4	44.3	34	6	BD248992	BD248992
44.3	24	6	BD084848	AX535397 Sequence	C 620	12.4	44.3	34	6	BD248992	BD248992
44.3	25	6	AX532762	BD084848 Modified	C 621	12.4	44.3	35	6	AR374091	AR374091
44.3	25	6	AX532763	AX532762 Sequence	C 622	12.4	44.3	35	6	A71940	A71940
44.3	25	6	AX609296	AX532763 Sequence	C 623	12.4	44.3	35	6	AR013969	AR013969
44.3	25	6	AX674949	AX609296 Sequence	C 624	12.4	44.3	35	6	AR147128	AR147128
44.3	27	6	AX172822	AX674949 Sequence	C 625	12.4	44.3	35	6	E06663	E06663
44.3	28	6	AX040958	AX172822 Sequence	C 626	12.4	44.3	35	6	I25584	I25584
44.3	29	6	AR014455	AX040958 Sequence	C 627	12.4	44.3	35	6	AR236289	AR236289
44.3	29	6	AX172824	AR014455 Sequence	C 628	12.4	44.3	35	6	BD009816	BD009816
44.3	30	6	AR011860	AX172824 Sequence	C 629	12.4	44.3	36	6	BD251194	BD251194
44.3	30	6	AR129097	AR011860 Sequence	C 630	12.4	44.3	36	6	AX172829	AX172829
44.3	30	6	BD243448	AR129097 Sequence	C 631	12.4	44.3	38	6	AR070957	AR070957
44.3	30	6	I71783	BD243448 Nucleic a	C 632	12.4	44.3	38	6	AX219312	AX219312
44.3	30	6	AX172825	I71783 Sequence 55	C 633	12.4	44.3	39	6	AR002612	AR002612
44.3	30	6	AX280502	AX172825 Sequence	C 634	12.4	44.3	39	6	AR099662	AR099662
44.3	30	6	AX361077	AX280502 Sequence	C 635	12.4	44.3	40	6	AR006865	AR006865
44.3	30	6	AX377765	AX361077 Sequence	C 636	12.4	44.3	40	6	AR081345	AR081345
44.3	30	6	AX791897	AX377765 Sequence	C 637	12.4	44.3	40	6	AR110889	AR110889
44.3	30	6	AX792486	AX791897 Sequence	C 638	12.4	44.3	40	6	I42324	I42324
44.3	30	6	AX792508	AX792486 Sequence	C 639	12.4	44.3	40	6	I73551	I73551
44.3	30	6	AX793272	AX792508 Sequence	C 640	12.4	44.3	40	6	I74805	I74805
44.3	30	6	AX793282	AX793272 Sequence	C 641	12.4	44.3	40	6	AX538355	AX538355
44.3	31	6	AR076337	AX793282 Sequence	C 642	12.4	44.3	40	6	AX538495	AX538495
44.3	31	6	AR090118	AR076337 Sequence	C 643	12.4	44.3	40	6	AX538500	AX538500
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ALIGNMENTS

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1634.1 GI:7241763

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unclassified.
 1 (bases 1 to 20)
 Damert, A. and Plate, K.
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 AND USE THEREOF
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 1 (bases 1 to 20)
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 HETEROLOGOUS DNA SEQUENCE IN ENDOTHELIAL CELLS IN VIVO
 THEREOF
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 ARTEMIS Pharmaceuticals GmbH (DE)
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TCTCTGCATGGTCAGGTC 20

95919 20 bp DNA linear PAT 17-JUL-2003
Library sequences capable of conferring expression of a
exologous DNA sequence in endothelial cells in vivo and uses
ref.

35919
25919.1 GI:33005689
2002511750-A/14.

Identified
classified.

(bases 1 to 20)

er.G., Risaui, W. and Ronicke, V.

Library sequences capable of conferring expression of a
exologous DNA sequence in endothelial cells in vivo and uses
nt: JP 2002511750-A 14 16-APR-2002;

PLANCK GESELLSCHAFT ZUR FORDERUNG DER WISSENSCHAFTEN EV

Unidentified

JP 2002511750-A/14

16-APR-2002

03-JUN-1998 JP 1999501504

03-JUN-1997 EP 97108959.4

GEORG BREIER, WERNER RISAUI, VOLKER RONICKE

C12N15/85, C12N15/12, C12N15/19, C07K14/47, C07K14/52, C12N15/58,

C12N9/72,

C12N15/53, C12N9/02, C12N15/23, C07K14/57, C12N15/16, C07K14/58, PC

2N5/10,

A61K48/00

Strandedness: Single;

Topology: linear;

/desc = 'oligonucleotide'

Key Location/Qualifiers

source 1..20

Location/Qualifiers

1..20

/organism="unidentified"

/mol_type="genomic DNA"

/db_xref="taxon:32644"

71.4%; Score 20; DB 6; Length 20;
Similarity 100.0%; Pred. No. 2.6e+02;
Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TCTCTGCATGGTCAGGTC 26

|||||

TCTCTGCATGGTCAGGTC 20

33 30 bp DNA linear PAT 26-JAN-2000
ance 9 from Patent WO9910500.

33.1 GI:6781697

KEYWORDS

unidentified

unidentified

unclassified.

REFERENCE 1 (bases 1 to 30)

AUTHORS Schlachter, U. and Steinbiss, H.

TITLE NUCLEIC ACID MOLECULES CODING FOR A CYSTEINE PROTEINASE

JOURNAL ORIGIN AND THEIR REGULATING REGIONS

Patent: WO 9910500-A 9 04-MAR-1999;

FEATURES MAX PLANCK GESELLSCHAFT (DE); SCHLACHTER URSULA (DE)

source

1..30

/organism="unidentified"

/mol_type="unassigned DNA"

/db_xref="taxon:32644"

ORIGIN

Query Match 64.3%; Score 18; DB 6; Length 30;
Best Local Similarity 80.8%; Pred. No. 2.3e+03;
Matches 21; Conservative 0; Mismatches 5; Indels 0;

QY 3 CATCATCTCTCTGCATGGTCAGGTCAT 28

|||||

Db 3 CATCTCATCTCTGCATGGTCAGGTCCT 28

RESULT 6

AX538397/c

LOCUS AX538397

DEFINITION Sequence 177 from Patent WO02072846.

ACCESSION AX538397

VERSION AX538397.1 GI:25270733

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Drocourt, D., Reynes, J.P. and Tiraby, G.

TITLE Synthetic genes and bacterial plasmids devoid of cpg

JOURNAL Patent: WO 02072846-A 177 19-SEP-2002;

FEATURES CAYLA (FR)

source

1..40

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="assembling oligo for CpG-free LacZ"

ORIGIN

Query Match 61.4%; Score 17.2; DB 6; Length 40;
Best Local Similarity 86.4%; Pred. No. 5.5e+03;
Matches 19; Conservative 0; Mismatches 3; Indels 0;

QY 1 AGCATCATCTCTCTGCATGGTCAT 22

|||||

Db 23 AGCACCACCTCTCTGCATGGACA 2

RESULT 7

AX538396

LOCUS AX538396

DEFINITION Sequence 176 from Patent WO02072846.

ACCESSION AX538396

VERSION AX538396.1 GI:25270732

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Drocourt, D., Reynes, J.P. and Tiraby, G.

TITLE Synthetic genes and bacterial plasmids devoid of cpg

JOURNAL Patent: WO 02072846-A 176 19-SEP-2002;

FEATURES CAYLA (FR)

Location/Qualifiers

1. .40
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Similarity 60.7%; Score 17; DB 6; Length 40;
 ; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

ATCATCCTCTGCATGTCAGGTCA 28

ACCACTCTCTGCATGACACAGTAT 25

717 nence 7 from Patent WO9322440. linear PAT 15-OCT-1999
 717 717.1 GI:6065688

identified
 identified
 lassified.
 (bases 1 to 29)

.,B. and Yap,E.

IA SEQUENCE OF DENGUE VIRUS SEROTYPE 1 (SINGAPORE STRAIN)

ent: WO 9322440-A 7 11-NOV-1993;

BOON HUAN (SG); YAP EU HIAN (SG)

Location/Qualifiers

1. .29
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/mol_type="unassigned DNA"

/db_xref="taxon:32644"

ilarity 57.1%; Score 16; DB 6; Length 29;
 Conservative 0; Mismatches 5; Indels 0; Gaps 0;

SCATCATCCTCTGCATGTCAGG 24

TCAGAAATTCCTGCAGGGTCAGG 25

337 337 nucleotide for PCR. 29 bp DNA linear PAT 29-SEP-1997
 337 337.1 GI:2175019

1994070760-A/6.

hctic construct

hctic construct

ificial sequences.

(bases 1 to 29)

irin,F., Buunnfuan,T., Iuuhian,Y., Youuchiyan,C. and Innuii,T.

RUE VIRUS

ent: JP 1994070760-A 6 15-MAR-1994;

VRIN FUU, BUUNNFUAN TAN, IUUHIAN YAFU, YOUUCHIYON CHIYAN, IN UII

Artificial gene

Artificial sequence; Genes.

JP 1994070760-A/6

15-MAR-1994

30-APR-1993 JP 1993127968

30-APR-1992 JP 92P 137717

JIANRIN FUU, BUUNNFUAN TAN, IUUHIAN YAFU, YOUUCHIYON CHIYAN,

INNUII TAN

C12N7/00,A61K39/12,C07K7/10,C07K13/00,C12N1/21,C12N5/10, PC

C12N7/04,C12N15/40,
 PC C12N15/62,C12P21/02,G01N33/53,G01N33/569,(C12N1/2

PC (C12P21/02,

PC C12R1:19),C07K99:00;

CC strandedness: Single;

CC topology: Linear.

FEATURES

source

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/mol_type="genomic DNA"

/db_xref="taxon:32630"

ORIGIN

Query Match 57.1%; Score 16; DB 6; Length 29;

Best Local Similarity 79.2%; Pred.No. 1.9e+04;

Matches 19; Conservative 0; Mismatches 5; Indels 0;

Qy 1 AGCATCATCCTCTGCATGTCAGG 24

Db 2 ATCAGAATTCCTGCAGGGTCAGG 25

RESULT 10

AX328821

LOCUS

DEFINITION AX328821 42 bp DNA linear PAT

Sequence 318 from Patent EP1164203.

ACCESSION AX328821

VERSION AX328821.1 GI:18102020

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

1. .42

/organism="unidentified"

/mol_type="unassigned DNA"

/db_xref="taxon:32644"

ORIGIN

Query Match

Best Local Similarity 57.1%; Score 16; DB 6; Length 42;

Matches 19; Conservative 0; Mismatches 5; Indels 0;

Qy 4 ATCATCCTCTGCATGTCAGGTCA 27

Db 1 ATCATCAACTGGAGATCAGGTCA 24

RESULT 11

BD132386

LOCUS

DEFINITION

BD132386

ACCESSION

BD132386.1 GI:23227331

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

PN JP 2002507883-A/318

PD 12-MAR-2002

PF 06-NOV-1997 JP 1998521832

BD132386

DNA diagnosis method based on mass spectrometry.

BD132386

JP 2002507883-A/318.

synthetic construct

artificial sequences.

1 (bases 1 to 42)

Koster,H., Little,D.P., Braun,A., Lough,D.M., Xiang,G.,

Boom,D.V.D., Jurinke,C. and Rupert,A.

DNA diagnosis method based on mass spectrometry

Patent: JP 2002507883-A 318 12-MAR-2002;

SEQUENOM INC

PN JP 2002507883-A/318

PD 12-MAR-2002

PF 06-NOV-1997 JP 1998521832

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06-NOV-1996 US 08/744481.06-NOV-1996 US 08/746036 PR
NOV-1996 US 08/746055.06-NOV-1996 US 08/744590 PR
JAN-1997 US 08/786988.23-JAN-1997 US 08/787639 PR
SEP-1997 US 08/933792.08-OCT-1997 US 08/947801 PI HUBERT
PER, DANIEL P LITTLE, ANDREAS BRAUN, DAVID M LOUGH, PI GUOBING
NG,
DIRK VAN DEN BOOM, CHRISTIAN JURINKE, ANDREAS RUPERT PC
21/68, C07H21/00, C07F9/24
Strandedness: Single;
Topology: Unknown;
Key Location/Qualifiers.
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  /db_xref="taxon:32630"
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  CATCCTCTGCATGCTCAGGTCA 27
  CATCACTGGAAGATCAGGTCA 24
  9517
  ence 14 from patent US 5891669.
  9517
  9517.1 GI:7220405
  OWN.
  OWN.
  assified.
  bases 1 to 30)
  en, E. Bech., Cherry, J.R. and Elrod, S.L.
  ods for producing polypeptides in respiratory-deficient cells
  nt: US 5891669-A 14 06-APR-1999;
  Location/Qualifiers
  1..30
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  /mol_type="unassigned DNA"
  55.7%; Score 15.6; DB 6; Length 30;
  ilarity 81.8%; Pred. No. 3e+04;
  Conservative 0; Mismatches 4; Indels 0; Gaps 0;
  CATCATCCTCTGCATGCTCA 22
  CGTCATCCTCTGCTTCGTCA 5
  5684
  ods for producing polypeptides in respiratory-deficient cells.
  5684
  5684.1 GI:33005454
  002510965-A/12.
  hetic construct
  hetic construct
  ficial sequences.
  bases 1 to 30)
  en, E. B., Cherry, J.R. and Elrod, S.L.
  ods for producing polypeptides in respiratory-deficient cells
  nt: JP 2002510965-A 12 09-APR-2002;
  NORDISK AS, NOVO NORDISK BIOTECH INC
  Artificial Sequence
  JP 2002510965-A/12

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PD 09-APR-2002
PF 17-MAR-1998 JP 1998540692
PR 17-MAR-1997 US 08/819458
PI EUNER BECH JENSEN, JOEL R CHERRY, SUSAN L ELROD PC
CL2N15/54, CL2P21/02, CL2N1/14//CL2R1/69
CC Aspergillus oryzae
CH Key Location/Qualifiers
  FT source 1..30
  FT /organism="Artificial Sequence".
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    Location/Qualifiers
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    /mol_type="genomic DNA"
    /db_xref="taxon:32630"
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    Query Match 55.7%; Score 15.6; DB 6; Length 30;
    Best Local Similarity 81.8%; Pred. No. 3e+04;
    Matches 18; Conservative 0; Mismatches 4; Indels 0;
    QY 1 AGCATCATCCTCTGCATGCTCA 22
    Db 26 ATCGTCATCCTCTGCTTCGTCA 5
  RESULT 14
  BD266770
  LOCUS
  DEFINITION
    33 bp DNA linear PAT
    Proteins that bind angiogenesis-inhibiting proteins, con
    and methods of use thereof.
  ACCESSION
  BD266770
  VERSION
  BD266770.1 GI:33076538
  KEYWORDS
  JP 2002532068-A/31.
  SOURCE
  synthetic construct
  ORGANISM
  synthetic construct
  artificial sequences.
  REFERENCE
  1 (bases 1 to 33)
  AUTHORS
  Macdonald, N.J. and Sim, K.L.
  TITLE
  Proteins that bind angiogenesis-inhibiting proteins, con
  and methods of use thereof
  JOURNAL
  Patent: JP 2002532068-A 31 02-OCT-2002;
  ENTREMED INC
  COMMENT
  OS Artificial Sequence
  PN JP 2002532068-A/31
  PD 02-OCT-2002
  PF 06-DEC-1999 JP 2000585271
  PR 04-DEC-1998 US 09/206059
  PI NICHOLAS J MACDONALD, KIM LEE SIM
  PC CL2N15/09, A61K38/00, A61P9/00, A61P27/02, A61P29/00, A6
  A61P43/00,
  PC C07K14/705, G01N33/15, G01N33/50, G01N33/53, G01N33/566//A61
  A61K45/00,
  PC A61K48/00, CL2N15/00, A61K37/02
  CC Synthetic binding peptide
  FH key Location/Qualifiers
  FT source 1..33
  FT /organism="Artificial Sequence".
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    Location/Qualifiers
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    /db_xref="taxon:32630"
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    Query Match 54.3%; Score 15.2; DB 6; Length 33;
    Best Local Similarity 85.0%; Pred. No. 4.6e+04;
    Matches 17; Conservative 0; Mismatches 3; Indels 0;
    QY 1 AGCATCATCCTCTGCATGCT 20
    Db 5 AGCTCTCATCTGCATGCT 24

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identified

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/mol_type="unassigned DNA"
/db_xref="taxon:32644"

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Conservative 0; Mismatches 8; Indels 0; Gaps 0;

GCATCATCTCTGCATGGTCAGGTCAT 28
|||||
GCGCCTCTTCAGCAGGTCATGGCTT 5

475
mer.
475
475.1 GI:5710158
1998072495-A/6.
identified
identified
classified.
(bases 1 to 56)
abayashi,T. and Sakano,S.
JNITY-RELATED FACTOR
nt: JP 1998072495-A 6 17-MAR-1998;
H CHEM IND CO LTD
None
Artificial sequences.
JP 1998072495-A/6
17-MAR-1998
11-JUN-1997 JP 1997153218
13-JUN-1996 JP 96P 152362
MIYABAYASHI TOMOYUKI, SAKANO SEIJI
COTK14/47,C07H21/04,C07K16/18,C12N5/10,C12N15/09, PC
21/02//A61K38/00,
C12P21/08, (C12N5/10, C12R1/91), (C12P21/02, C12R1/91), (C12P21/08,
C12R1/91);
strandedness: Single;
topology: Linear;
hypothesis: No;
Key Location/Qualifiers
source 1. .56
Location/Qualifiers
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CATCATCTCTGCATGGTCAGGTCAT 28
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7977
nce 34 from Patent WO0190747.
7977
7977.1 GI:18098132
netic construct
netic construct

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/db_xref="taxon:32644"

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Conservative 0; Mismatches 8; Indels 0; Gaps 0;

GCATCATCTCTGCATGGTCAGGTCAT 28
|||||
GCGCCTCTTCAGCAGGTCATGGCTT 5

475
mer.
475
475.1 GI:5710158
1998072495-A/6.
identified
identified
classified.
(bases 1 to 56)
abayashi,T. and Sakano,S.
JNITY-RELATED FACTOR
nt: JP 1998072495-A 6 17-MAR-1998;
H CHEM IND CO LTD
None
Artificial sequences.
JP 1998072495-A/6
17-MAR-1998
11-JUN-1997 JP 1997153218
13-JUN-1996 JP 96P 152362
MIYABAYASHI TOMOYUKI, SAKANO SEIJI
COTK14/47,C07H21/04,C07K16/18,C12N5/10,C12N15/09, PC
21/02//A61K38/00,
C12P21/08, (C12N5/10, C12R1/91), (C12P21/02, C12R1/91), (C12P21/08,
C12R1/91);
strandedness: Single;
topology: Linear;
hypothesis: No;
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Location/Qualifiers
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Conservative 0; Mismatches 8; Indels 0; Gaps 0;

CATCATCTCTGCATGGTCAGGTCAT 28
|||||
CATCATCATCTTTATATATCGGTCCT 42

7977
nce 34 from Patent WO0190747.
7977
7977.1 GI:18098132
netic construct
netic construct

artificial sequences.
1
Rhode,P., Wittman,V., Weidanz,J.A., Burkhardt,M., Card,
Tal,R., Acevedo,J. and Wong,H.C.
Modulation of t-cell receptor interactions
Patent: WO 0190747-A 34 29-NOV-2001;
Sunol Molecular Corporation (US)
Location/Qualifiers
source 1. .58
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

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Best Local Similarity 85.0%; Pred. No. 4.8e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0;

QY 6 CATCTCTCTGCATGGTCAGGT 25
|||||
DB 53 CATCTCTCTGTGTGTCTAGGT 34
|||||

RESULT 22
AX254656
LOCUS
DEFINITION Sequence 12 from Patent WO0168818.
ACCESSION AX254656
VERSION AX254656.1 GI:16074328
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
1
Steinkuhler,C.I., Pallaro,M.I. and Lahm,A.I.
Hcv ns2/3 fragments and uses thereof
Patent: WO 0168818-A 12 20-SEP-2001;
Istituto di Ricerche di Biologia Molecolare P. Angelelli;
Location/Qualifiers
source 1. .44
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"

Query Match 53.6%; Score 15; DB 6; Length 44;
Best Local Similarity 78.3%; Pred. No. 5.8e+04;
Matches 18; Conservative 0; Mismatches 5; Indels 0;

QY 2 GCATCATCTCTGCATGGTCAGG 24
|||||
DB 2 GCATCATCATCATCATCATCAGG 24
|||||

RESULT 23
BD002886/c
LOCUS
DEFINITION Gene composition and method.
ACCESSION BD002886
VERSION BD002886.1 GI:18630847
KEYWORDS JP 2000245487-A/552.
SOURCE
ORGANISM
unidentified
unclassified.
1 (bases 1 to 31)
REFERENCE
AUTHORS Sha,N., Walinton,J. and Patel,N.
TITLE Gene composition and method
JOURNAL Patent: JP 2000245487-A 552 12-SEP-2000;
AFIMETRICS INC
COMMENT OS Unknown
EN JP 2000245487-A/552

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12-SEP-2000
27-JAN-2000 JP 2000019392
27-JAN-1999 US 09/238,402
NIRA SHA, JANET WALINTON, NIRA PATEL
C12N15/09, C12Q1/68, C12N15/00

Key Location/Qualifiers
source 1..31
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milarity 52.9%; Score 14.8; DB 6; Length 31;
Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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GCCTCTGCTCTGCATTGT 3

618 40 bp DNA linear PAT 21-JAN-2000
ence 47 from Patent WO9849324.
618

618.1 GI:6732870

Identified
Identified
lassified.
(bases 1 to 40)
-his, G.

BOHYDRATE-DEFICIENT GLYCOPROTEIN SYNDROME TYPE I
ent: WO 9849324-A 47 05-NOV-1998;
THIS GER (BE); GENZYME LTD (GB)

Location/Qualifiers
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milarity 52.9%; Score 14.8; DB 6; Length 40;
Conservative 0; Mismatches 7; Indels 0; Gaps 0;

TATCATCTCTGCATGGTCAGTCA 27
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TTCTTGCTGATGGTCTGGCCA 4

38134 46 bp DNA linear PAT 14-FEB-2003
ence 408 from Patent WO0244994.
38134
38134.1 GI:28398308

thetic construct
thetic construct
ificial sequences.

ver A., Brow, M.A., Cracauer, R.F., Fors, L., Granske, R., de arruda
ig, M., Kurensky, D., Luedtke, C., Lukowiak, A.A., Lyamichev, V.,
B.P., Reimer, N.B., Roewen, R.T., Skrzypczynski, Z., Ziarno, W.A.,
rford, S., Stump, S. and Viegut, D.D.
tems and method for detection assay production and sale
nt: WO 0244994-A 408 06-JUN-2002;

THIRD WAVE TECHNOLOGIES, INC. (US)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN

Query Match 52.9%; Score 14.8; DB 6; Length 46;
Best Local Similarity 73.1%; Pred. No. 7.2e+04;
Matches 19; Conservative 0; Mismatches 7; Indels 0;
QY 1 AGCATCATCTCTGCATGGTCAGGTC 26
|||||
Db 26 AGCATCATATTGTCAGACAGGAC 1

RESULT 26
AR148167

LOCUS 50 bp DNA linear PAT
DEFINITION Sequence 13 from patent US 6225063.
ACCESSION AR148167
VERSION AR148167.1 GI:15112257
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 50)
AUTHORS Khvorova, A. and Varus, M.
TITLE RNA channels in biological membranes
JOURNAL Patent: US 6225063-A 13 01-MAY-2001;
FEATURES
source 1..50
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 52.9%; Score 14.8; DB 6; Length 50;
Best Local Similarity 73.1%; Pred. No. 7.2e+04;
Matches 19; Conservative 0; Mismatches 7; Indels 0;

QY 1 AGCATCATCTCTGCATGGTCAGGTC 26
|||||
Db 7 ATCTTAATTCTGCGTGGTCAGGTC 32

RESULT 27
AX157925

LOCUS 51 bp DNA linear PAT
DEFINITION Sequence 1253 from Patent WO0140521.
ACCESSION AX157925
VERSION AX157925.1 GI:14539256
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS

TITLE Shimke's, R.A. and Leach, M.
Nucleic acids containing single nucleotide polymorphisms
Methods of use thereof
JOURNAL Patent: WO 0140521-A 1253 07-JUN-2001;
Curagen Corporation (US)
FEATURES
source 1..51
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

misc_feature

26
/note="1 of 2 allelic variants (1254 is other €
Accession number cg28473092"

ORIGIN

X., Fernandes, E., Li, L., Kekuda, R., Liu, Y., Leite, M., Lek, K.A., Ji, W., Casman, S. J., Boldog, F. L., Patturajan, M., Reck, C.A., Ballinger, R.A., Malyankar, U.M., Tchervnev, V.T., Stock, A.D., Gusev, V.Y., Rastelli, L., Mezes, P.D., Ellerman, K., Smith, M., Herrmann, J. L., Shimkets, R.A., Toime, N., Pena, C.E., Oyler, S.C., Taupier, R.J., Gerlach, V. and Gorman, L. In proteins and nucleic acids encoding same nt: WO 0209817-A 479 12-DEC-2002; gen Corporation (US)

REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES

52.1%; Score 14.6; DB 6; Length 40;
 milarity 81.0%; Pred. No. 8.9e+04;
 Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ATCATCCTCTGCATGGTCA 22
 ||| ||||| ||||| |||||
 ACACCTGCTCTACATGGTCA 13

34368 45 bp DNA linear PAT 11-SEP-2001
 uence 18 from Patent WO0162942.

34368
 34368.1 GI:15593369

thetic construct
 thetic construct
 ificial sequences.

talo, K.M. and Jeltsch, M.M.
 erials and methods involving hybrid vascular endothelial growth
 tor dnas and proteins and screening methods for modulators
 ent: WO 0162942-A 18 30-AUG-2001;
 NIG INSTITUTE FOR CANCER RESEARCH (US); Licentia OY (FI)

1. .45
 Location/Qualifiers
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52.1%; Score 14.6; DB 6; Length 45;
 milarity 81.0%; Pred. No. 8.9e+04;
 Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ATCCTCTGCATGGTCA 25
 ||| ||||| ||||| |||||
 ATATATCTGCATGGTCA 26

14359 45 bp DNA linear PAT 11-SEP-2001
 uence 9 from Patent WO0162942.

14359
 14359.1 GI:15593360

thetic construct
 thetic construct
 ificial sequences.

talo, K.M. and Jeltsch, M.M.
 erials and methods involving hybrid vascular endothelial growth
 or dnas and proteins and screening methods for modulators
 nt: WO 0162942-A 9 30-AUG-2001;
 NIG INSTITUTE FOR CANCER RESEARCH (US); Licentia OY (FI)

1. .46
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ATCCTCTGCATGGTCA 25

Db 45 TCATAATCTGCATGGTCA 25
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 LOCUS AX165131 DNA linear PA
 DEFINITION Sequence 326 from Patent WO0138586.
 ACCESSION AX165131
 VERSION AX165131.1 GI:14545960
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Hc

REFERENCE 1
 AUTHORS Shimkets, R.A. and Leach, M.
 TITLE Nucleic acids containing single nucleotide polymorphism
 JOURNAL methods of use thereof
 PATENT: WO 0138586-A 326 31-MAY-2001;
 Curagen Corporation (US)

FEATURES
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 Accession number cg43930957"

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Db 49 ATCCTCTGCATGGTCA 29
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RESULT 35
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LOCUS AR028646 26 bp DNA linear PAT
 DEFINITION Sequence 14 from patent US 5858740.
 ACCESSION AR028646
 VERSION AR028646.1 GI:5940619

KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1. (bases 1 to 26)
 AUTHORS Finer, M.H.; Roberts, M.R.; Dull, T.J.; Zsebo, K.M.; Qin, L.
 TITLE Method for production of high titer virus and high effi
 JOURNAL retroviral mediated transduction of mammalian cells
 PATENT: US 5858740-A 14 12-JAN-1999;
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53739 26 bp DNA linear PAT 29-SEP-1999
 53739 14 from patent US 5834256.
 53739.1 GI:5978601

nown.

lassified.
 (bases 1 to 26)

er,M.H., Roberts,M.R., Dull,T.J., Zsebo,K.M., Qin,L. and
 son,D.A.
 nod for production of high titer virus and high efficiency
 rovirai mediated transduction of mammalian cells
 ent: US 5834256-A 14 10-NOV-1998;
 Location/Qualifiers

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TATCCTTCGATGTCAGGTCAT 28
 TACCTTCTTCAAGGTCAGATCTT 2

6239 26 bp DNA linear PAT 08-AUG-2001
 6239 14 from patent US 6218187.
 6239.1 GI:15109428

nown.

assified.
 bases 1 to 26)

ar,M.H., Dull,T.J., Zsebo,K.M., Cooke,K. and Farson,D.A.
 od for production of high titer virus and high efficiency
 rovirai mediated transduction of mammalian cells
 nt: US 6218187-A 14 17-APR-2001;
 Location/Qualifiers

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8189 26 bp DNA linear PAT 20-APR-2002
 8189 8 from patent US 6319494.
 8189.1 GI:20219327

OWN.

assified.
 bases 1 to 26)

n,D.J., Weiss,A., Irving,B.A., Roberts,M.R. and Zsebo,K.
 eric chains for receptor-associated signal transduction
 ways

JOURNAL Patent: US 6319494-A 8 20-NOV-2001;
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ORIGIN

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 Db 25 TCACCTTCTTCAAGGTCAGATCTT 2

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 ACCESSION I73318
 VERSION I73318.1 GI:3009457
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 26)
 AUTHORS Finer,M.H., Roberts,M.R., Dull,T.J., Zsebo,K.M., Qin,L.
 TITLE Method for production of high titer virus and high effi
 retroviral mediated transduction of mammalian cells
 Patent: US 5686279-A 14 11-NOV-1997;
 Location/Qualifiers

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ORIGIN

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RESULT 40
 AR214471/c

LOCUS 26 bp mRNA linear PAT
 DEFINITION Sequence 8 from patent US 6407221.
 ACCESSION AR214471
 VERSION AR214471.1 GI:23312296
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 26)
 AUTHORS Capon,D.J., Weiss,A., Irving,B.A., Roberts,M.R. and Zseb
 Chimeric chains for receptor-associated signal transduct
 pathways
 Patent: US 6407221-A 8 18-JUN-2002;
 Location/Qualifiers

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ORIGIN

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QY 5 TCATCCTTCGATGTCAGGTCAT 28

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GenCore version 5.1.6
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April 12, 2004, 19:19:44 ; Search time 82.3077 Seconds
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US-10-090-326-23

28

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IDENTITY NUC

Gapop 10.0 , Gapext 1.0

2475585 seqs, 1875730760 residues

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length: 0

length: 60

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Maximum Match 100%

Listing first 1000 summaries

Published Applications NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US05_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
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- 9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
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- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
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- 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

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rived by analysis of the total score distribution.

SUMMARIES

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54.3	60	10	US-09-908-975-20184		Sequence 20184, A
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US-10-014-099F-102
; Sequence 102, Application US/10014099F
; Publication No. US20040003420A1
; GENERAL INFORMATION:
; APPLICANT: KUEHN, Ralf
; APPLICANT: FELDER, Susanne
; APPLICANT: SCHWENK, Frieder
; APPLICANT: KUETER-LUKS, Birgit
; APPLICANT: FAUST, Nicole
; TITLE OF INVENTION: Modified Recombinase
; FILE REFERENCE: 012787wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/014,099F
; CURRENT FILING DATE: 2001-11-12
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 102
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; OTHER INFORMATION: beta-Gal 3
US-10-014-099F-102

```

Application US/10359050
US20030186291A1

```

1  ; APPLICANT: FAIGLER, Simonon
2  ; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRJ
3  ; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
4  ; FILE REFERENCE: 36688-0005
5  ; CURRENT APPLICATION NUMBER: US/09/908,975
6  ; CURRENT FILING DATE: 2001-07-20
7  ; PRIOR APPLICATION NUMBER: US 60/287,724
8  ; PRIOR FILING DATE: 2001-05-02
9  ; PRIOR APPLICATION NUMBER: US 60/221,607
10 ; PRIOR FILING DATE: 2000-07-28
11 ; NUMBER OF SEQ ID NOS: 32337
12 ; SOFTWARE: PatentIn version 3.0
13 ; SEQ ID NO 22950
14 ; LENGTH: 60
15 ; TYPE: DNA
16 ; ORGANISM: Homo sapiens
17 ; US-09-908-975-22950

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Best Local Similarity	77.8%;	Pred. No. 5.9e+02;		
Matches 21;	Conservative	0;	Mismatches 6;	Indels 0;

RESULT 4

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; Sequence 21137, Application US/09908975
; Publication No. US20030165843A1

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; APPLICATION NUMBER: 08/744,590
; FILING DATE: 06-NO. US20020042112A1-96
; APPLICATION NUMBER: 08/744,481
; FILING DATE: 06-NO. US20020042112A1-96
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24736-2004B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-450-8400
; TELEFAX: 858-587-5360
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 318:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 318:
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US-09-179-536B-318

Query Match 57.1%; Score 16; DB 9; Length 42;
Best Local Similarity 79.2%; Pred. No. 2.3e+03;
Matches 19; Conservative 0; Mismatches 5; Indels 0;

QY 4 ATCATCCTCGCATGTCAGGTCA 27
Db 1 ATCATCACTGGAAGATCAGGTCA 24

RESULT 6
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; Sequence 318, Application US/09297576A
; Publication No. US20030129589A1
; GENERAL INFORMATION:
; APPLICANT: KOSTER, Hubert
; APPLICANT: LITTLE, Daniel P.
; APPLICANT: BRAUN, Andreas
; APPLICANT: LOUGH, David M.
; APPLICANT: XIANG, Guobing
; APPLICANT: VAN DEN BOOM, Dirk
; APPLICANT: JURINKE, Christian
; APPLICANT: RUPPERT, Andreas
; TITLE OF INVENTION: DNA DIAGNOSTICS BASED ON MASS SPECTROMETRY
; NUMBER OF SEQUENCES: 320
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; FILING APPLICATION NUMBER: US/09/297,576A
; FILING DATE: 07-Jun-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/947,801
; FILING DATE: 08-Oct-97
; APPLICATION NUMBER: 08/933,792
; FILING DATE: 19-Sep-97
; APPLICATION NUMBER: 08/787,639
; FILING DATE: 23-Jan-97

```

ION NUMBER: 08/786,988
ATE: 23-Jan-97
ION NUMBER: 08/746,055
ATE: 06-NO. US20030129589A1-96
ION NUMBER: 08/746,036
ATE: 06-NO. US20030129589A1-96
ION NUMBER: 08/744,590
ATE: 06-NO. US20030129589A1-96
ION NUMBER: 08/744,481
ATE: 06-NO. US20030129589A1-96
BENT INFORMATION:
aidman, Stephanie L.
ION NUMBER: 33,779
3/DOCKET NUMBER: 24736-2004
ICATION INFORMATION:
858-450-8499
FOR SEQ ID NO: 318:
HARACTERISTICS:
42 base pairs
nucleic acid
MESS: single
: unknown
EPE: cDNA
AL: NO
: NO
EPE: <Unknown>
SOURCE:
118

57.1%; Score 16; DB 10; Length 42;
similarity 79.2%; Pred. No. 2.3e+03;
Conservative 0; Mismatches 5; Indels 0; Gaps 0;
TCATCCTCTGCAATGTCAGGTCA 27
||||| ||||| ||||| ||||| |||||
TCATCAACTGGAGATCAGGTCA 24

309/c
Application US/09908975
US20030165843A1
ATION:
OSHAN, Avi
WASSERMAN, Alon
MINTZ, Eli
MINTZ, Liat
AIGLER, Simchon
ENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
ENTION: THAT POPULATE A TRANSCRIPTOME
E: 36688-0005
ATION NUMBER: US/09/908,975
G DATE: 2001-07-20
ATION NUMBER: US 60/287,724
DATE: 2001-05-02
ATION NUMBER: US 60/221,607
DATE: 2000-07-28
Q ID NOS: 32337
entIn version 3.0
)

omo sapiens
309
55.0%; Score 15.4; DB 10; Length 60;
similarity 94.1%; Pred. No. 4.3e+03;
Conservative 0; Mismatches 1; Indels 0; Gaps 0;
TCTGCAATGTCAGGT 25
||||| ||||| ||||| ||||| |||||
TCTGCAATGTCAGGT 33

RESULT 8
US-09-908-975-12691
Sequence 12691, Application US/09908975
Publication No. US20030165843A1
GENERAL INFORMATION:
APPLICANT: SHOSHAN, Avi
APPLICANT: WASSERMAN, Alon
APPLICANT: MINTZ, Eli
APPLICANT: MINTZ, Liat
APPLICANT: FAIGLER, Simchon
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TR
FILE REFERENCE: 36688-0005
CURRENT APPLICATION NUMBER: US/09/908,975
CURRENT FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 60/287,724
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/221,607
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 32337
SOFTWARE: PatentIn version 3.0
SEQ ID NO 12691
LENGTH: 60
TYPE: DNA
ORGANISM: Homo sapiens
US-09-908-975-12691

Query Match 55.0%; Score 15.4; DB 10; Length 60;
Best Local Similarity 76.0%; Pred. No. 4.3e+03;
Matches 19; Conservative 0; Mismatches 6; Indels 0;
QY 3 CATCATCCTCTGCAATGTCAGGTCA 27
||||| ||||| ||||| ||||| |||||
DB 36 CATGGGCGCTCTACATCGTCAGGACA 60

RESULT 9
US-09-873-676-71
Sequence 71, Application US/09873676
Patent No. US20020077289A1
GENERAL INFORMATION:
APPLICANT: MacDonald, Nicholas J.
TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins
FILE REFERENCE: 05213-0378 (43170-259333)
CURRENT APPLICATION NUMBER: US/09/873,676
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: US 60/209,065
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: US 60/289,387
PRIOR FILING DATE: 2001-05-08
NUMBER OF SEQ ID NOS: 123
SOFTWARE: PatentIn version 3.1
SEQ ID NO 71
LENGTH: 33
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: binding molecule
US-09-873-676-71

Query Match 54.3%; Score 15.2; DB 9; Length 33;
Best Local Similarity 85.0%; Pred. No. 5e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0;
QY 1 AGCATCATCCTCTGCAATGCT 20
||||| ||||| ||||| ||||| |||||
DB 5 AGCCTCCTCATCTGCAATGCT 24
RESULT 10

Application US/10403980
US20030176351A1

ATION:

SEWICZ, SUSAN

SPOM, GERALD T.

EPOM, BARBARA S.

ATION: PEPTIDES AND PEPTIDE ANALOGUES DESIGNED FROM A
TION: DIABETES-ASSOCIATED AUTOANTIGEN, AND METHODS FOR THEIR
ATION: USE IN THE TREATMENT AND PREVENTION OF DIABETES

E: 20149-1-1

CATION NUMBER: US/10/403,980

3 DATE: 2003-03-28

TION NUMBER: 09/379,211

DATE: 1999-08-23

ID NOS: 29

entIn Ver. 2.1

tificial Sequence

ATION: Description of Artificial Sequence: HLA-DR4

ATION: binding peptide encoding SEQ ID NO: 1.

ilarity 54.3%; Score 15.2; DB 14; Length 39;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CTCTGCGATGTCAGGTCA 27

TTCCGCGATGTCAGGTCA 24

184

, Application US/09908975

. US20030165843A1

ATION:

OSHAN, Avi

ASSERMAN, Alon

INTZ, Eli

INTZ, Liat

AGLER, Simchon

ATION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE

ATION: THAT POPULATE A TRANSCRIPTOME

E: 36688-0005

CATION NUMBER: US/09/908,975

G DATE: 2001-07-20

TION NUMBER: US 60/287,724

DATE: 2001-05-02

TION NUMBER: US 60/221,607

DATE: 2000-07-28

ID NOS: 32337

entIn version 3.0

4

mo sapiens

184

ilarity 54.3%; Score 15.2; DB 10; Length 60;

Conservative 0; Mismatches 3; Indels 0; Gaps 0;

TTCCTCTGCGATGTCAGT 25

TTCCACTGCTTGGTCAGT 37

236

; Sequence 9236, Application US/10098263B

; Publication No. US20030104410A1

; GENERAL INFORMATION:

; APPLICANT: Mittman, Michael

; TITLE OF INVENTION: Human Microarray

; FILE REFERENCE: 3118.1

; CURRENT APPLICATION NUMBER: US/10/098,263B

; CURRENT FILING DATE: 2003-01-08

; PRIOR APPLICATION NUMBER: 60/276,759

; PRIOR FILING DATE: 2001-03-16

; NUMBER OF SEQ ID NOS: 131066

; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

; SEQ ID NO 9236

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Homo sapien

US-10-098-263B-9236

Query Match

53.6%; Score 15; DB 14; Length 25;

Best Local Similarity 78.3%; Pred. No. 6e+03;

Matches 18; Conservative 0; Mismatches 5; Indels 0;

QY 6 CATCCTCTGCGATGTCAGGTCA 28

DB 3 CGTTCCTTCATAGTCAGGGCAT 25

RESULT 13

US-10-221-943-12

; Sequence 12, Application US/10221943

; Publication No. US20040054134A1

; GENERAL INFORMATION:

; APPLICANT: Steinkuhler, Christian

; APPLICANT: Pallao, Michele

; APPLICANT: Lahm, Armin

; TITLE OF INVENTION: HCV NS2/3 FRAGMENTS AND USES THEREOF

; FILE REFERENCE: IT0031P

; CURRENT APPLICATION NUMBER: US/10/221,943

; CURRENT FILING DATE: 2002-09-17

; PRIOR APPLICATION NUMBER: PCT/IB01/0052

; PRIOR FILING DATE: 2001-03-14

; PRIOR APPLICATION NUMBER: GB 0006537.5

; PRIOR FILING DATE: 2000-03-17

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12

; LENGTH: 44

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Primer

US-10-221-943-12

Query Match

53.6%; Score 15; DB 12; Length 44;

Best Local Similarity 78.3%; Pred. No. 6.3e+03;

Matches 18; Conservative 0; Mismatches 5; Indels 0;

QY 2 GCATCATCTCTGCGATGTCAGG 24

DB 2 GCATCATCATCATCATCATCAGG 24

RESULT 14

US-03-908-975-31738/c

; Sequence 31738, Application US/09908975

; Publication No. US20030165843A1

; GENERAL INFORMATION:

; APPLICANT: SHOSHAN, Avi

; APPLICANT: WASSERMAN, Alon

; APPLICANT: MINTZ, Eli

; APPLICANT: MINTZ, Liat

; APPLICANT: FAIGLER, Simchon

; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRA

3 09:04:21 2004

us-10-090-326-23.max.rnpb

ENTION: THAT POPULATE A TRANSCRIPTOME

CE: 36688-0005
ICATION NUMBER: US/09/908,975
NG DATE: 2001-07-20
ATION NUMBER: US 60/287,724
DATE: 2001-05-02
ATION NUMBER: US 60/221,607
DATE: 2000-07-28
Q ID NOS: 32337
tentIn version 3.0
38

omo sapiens
1738

53.6%; Score 15; DB 10; Length 60;
milarity 78.3%; Pred. No. 6.4e+03;
Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CATCATCTCTGCATGTCAGG 24
||||| ||||| ||||| |||||
CATCACCATCTTCATGTTGAGG 3

1858/c
8, Application US/09908975
O. US20030165843A1

MATION:
WASSERMAN, Alon
HOSHAN, Avi
MINTZ, Eli
MINTZ, Liat

ENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
ENTION: THAT POPULATE A TRANSCRIPTOME

CE: 36688-0005
ICATION NUMBER: US/09/908,975
NG DATE: 2001-07-20
ATION NUMBER: US 60/287,724
DATE: 2001-05-02
ATION NUMBER: US 60/221,607
DATE: 2000-07-28
Q ID NOS: 32337
tentIn version 3.0
58

omo sapiens
1858

53.6%; Score 15; DB 10; Length 60;
milarity 78.3%; Pred. No. 6.4e+03;
Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CATCATCTCTGCATGTCAGG 24
||||| ||||| ||||| |||||
CATCACCATCTTCATGTTGAGG 3

19509/c
9, Application US/10098263B
O. US20030104410A1

MATION:
ittman, Michael
ENTION: Human Microarray

CE: 3118.1
ICATION NUMBER: US/10/098,263B
NG DATE: 2003-01-08
ATION NUMBER: 60/276,759
DATE: 2001-03-16

; NUMBER OF SEQ ID NOS: 131066
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 19509
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-19509

Query Match 52.9%; Score 14.8; DB 14; Length 25;
Best Local Similarity 88.9%; Pred. No. 7.3e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0;

Qy 9 CCTCTGCATGTCAGGTC 26
||||| ||||| ||||| |||||
Db 25 CCTCTGCATGTCAGGTC 8

RESULT 17

US-10-321-039-297/c
; Sequence 297, Application US/10321039
; Publication No. US20040014067A1
; GENERAL INFORMATION:
; APPLICANT: Lyamichev, Victor
; APPLICANT: Lukowiak, Andrew
; APPLICANT: Jarvis, Nancy
; APPLICANT: Kurensky, David
; TITLE OF INVENTION: Amplification Methods and Compositions
; FILE REFERENCE: FORS-06960
; CURRENT APPLICATION NUMBER: US/10/321,039
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: 09/998,157
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/329,113
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/360,489
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 759
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 297
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-321-039-297

Query Match 52.9%; Score 14.8; DB 15; Length 46;
Best Local Similarity 73.1%; Pred. No. 7.7e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0;

Qy 1 AGCATCATCTCTGCATGTCAGGTC 26
||||| ||||| ||||| |||||
Db 26 AGCATCATCTCTGCATGTCAGGTC 1

RESULT 18

US-10-131-827-1808
; Sequence 1808, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 50661200120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08

Q ID NOS: 9090
tentIn version 3.1
16

lomo sapiens
808

52.9%; Score 14.8; DB 15; Length 50;
milarity 88.9%; Pred. No. 7.7e+03;
Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CTGCATGGTCAGGTGAT 28
|||||
CTGCATGGTAATGTCAT 40

3378/c

, Application US/10282122A
O. US20040029129A1

MATION:
ang, Liangsu
Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Irawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
Xu, H.

ENTION: Identification of Essential Genes in Microorganisms

SE: ELITRA.034A

ICATION NUMBER: US/10/282,122A

NG DATE: 2003-02-20

ATION NUMBER: 60/191,078

DATE: 2000-03-21

ATION NUMBER: 60/206,848

DATE: 2000-05-23

ATION NUMBER: 60/207,727

DATE: 2000-05-26

ATION NUMBER: 60/230,335

DATE: 2000-09-06

ATION NUMBER: 60/230,347

DATE: 2000-09-09

ATION NUMBER: 60/242,578

DATE: 2000-10-23

ATION NUMBER: 60/253,625

DATE: 2000-11-27

ATION NUMBER: 60/257,931

DATE: 2000-12-22

ATION NUMBER: 60/267,636

DATE: 2001-02-09

ATION NUMBER: 60/269,308

DATE: 2001-02-16

or Application data removed - See File Wrapper or PALM.

Q ID NOS: 78614

tentIn version 3.1

cherichia coli
1378

52.9%; Score 14.8; DB 12; Length 53;
milarity 73.1%; Pred. No. 7.7e+03;
Conservative 0; Mismatches 7; Indels 0; Gaps 0;

ICATCATCCTCTGCATGGTCAGGTC 26
||||| ||| ||| ||| |||

Db 28 AGCATCAAGCTCAGCAACGTGAAGTC 3

RESULT 20

US-09-908-975-16241/c

; Sequence 16241, Application US/09908975

; Publication No. US20030165843A1

; GENERAL INFORMATION:

; APPLICANT: SHOSHAN, Avi

; APPLICANT: WASSERMAN, Alon

; APPLICANT: MINTZ, Eli

; APPLICANT: MINTZ, Liat

; APPLICANT: FAISLER, Simchon

; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TR

; FILE REFERENCE: 36688-0005

; CURRENT APPLICATION NUMBER: US/09/908,975

; PRIOR FILING DATE: 2001-07-20

; PRIOR APPLICATION NUMBER: US 60/287,724

; PRIOR FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: US 60/221,607

; PRIOR FILING DATE: 2000-07-28

; NUMBER OF SEQ ID NOS: 32337

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 16241

; LENGTH: 60

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-908-975-16241

Query Match 52.9%; Score 14.8; DB 10; Length 60;
Best Local Similarity 73.1%; Pred. No. 7.8e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0;

QY 2 GCATCATCTCTGCATGGTCAGGTCA 27

Db 45 GCATCATCTCTGCATGGTAAGGAATTCA 20

RESULT 21

US-09-908-975-18696

; Sequence 18696, Application US/09908975

; Publication No. US20030165843A1

; GENERAL INFORMATION:

; APPLICANT: SHOSHAN, Avi

; APPLICANT: WASSERMAN, Alon

; APPLICANT: MINTZ, Eli

; APPLICANT: MINTZ, Liat

; APPLICANT: FAISLER, Simchon

; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TR

; FILE REFERENCE: 36688-0005

; CURRENT APPLICATION NUMBER: US/09/908,975

; PRIOR FILING DATE: 2001-07-20

; PRIOR APPLICATION NUMBER: US 60/287,724

; PRIOR FILING DATE: 2001-05-02

; PRIOR APPLICATION NUMBER: US 60/221,607

; PRIOR FILING DATE: 2000-07-28

; NUMBER OF SEQ ID NOS: 32337

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 18696

; LENGTH: 60

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-908-975-18696

Query Match 52.9%; Score 14.8; DB 10; Length 60;
Best Local Similarity 73.1%; Pred. No. 7.8e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0;

QY 3 CATCATCTCTGCATGGTCAGGTCA 28

Db 2 CTTATCCACTCCATGCTCAGCACGT 27

US-10-074-978A-479

Query Match 52.1%; Score 14.6; DB 15; Length 22;
Best Local Similarity 81.0%; Pred No. 8.8e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0

QY 3 CATCATCCTCTGCATGTCAG 23
| | | | | | | | | | | | | | | | | | | |
Db 1 CCTCATCCTTTTCATGTCAG 21

RESULT 23

US-10-074-978A-482
; Sequence 482, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
; APPLICANT: Leite, Mario
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Fernandes, Elma
; APPLICANT: Li, Li
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Liu, Xiahong
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Patturajan, Meera
; APPLICANT: Blalock, Angela
; APPLICANT: Ballinger, Robert
; APPLICANT: Vernet, Corine
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter S
; APPLICANT: Ellerman, Karen
; APPLICANT: Heyes, Melvin P
; APPLICANT: Herzman, John
; APPLICANT: Pena, Carol E A
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Moore, No. US20040010119A11le
; APPLICANT: Shenoy, Suresh
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, Dave
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SP
; FILE REFERENCE: 21402-269
; CURRENT APPLICATION NUMBER: US/10/074,978A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: 60/268,221
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/335,109
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/312,284
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/268,496
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/276,703
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/330,293
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/322,127
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/280,899
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/310,797
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/268,646
; PRIOR FILING DATE: 2001-02-14
; Remaining Prior Application data removed - See File Wrapper or P

US-10-074-978A-479

Application US/10074978A
No. US20040010119A1
NATION:
eite, Mario
Spytek, Kimberly A
Guo, Xiaojia (Sasha)
Fernandes, Elma
Li, Li
Kekuda, Ramesh
Liu, Xiahong
Casman, Stacie
Boldog, Ferenc
Patturajan, Meera
Blalock, Angela
Ballinger, Robert
Vernet, Corine
Tchernev, Velizar T
Malyankar, Uriel M
Gusev, Vladimir
Rastelli, Luca
Mezes, Peter S
Ellerman, Karen
Heyes, Melvin P
Herzman, John
Pena, Carol E A
Shimkets, Richard A
Taupier Jr, Raymond J
Moore, No. US20040010119A11le
Shenoy, Suresh
Edingez, Shlomit
Gunther, Erik
Stone, Dave
Millet, Isabelle
Peyman, John
Smithson, Glenda
INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
ICE: 21402-269
ICATION NUMBER: US/10/074,978A
NG DATE: 2003-01-07
ATION NUMBER: 60/268,221
; DATE: 2001-02-12
ATION NUMBER: 60/335,109
; DATE: 2001-10-31
ATION NUMBER: 60/312,284
; DATE: 2001-08-14
ATION NUMBER: 60/268,496
; DATE: 2001-02-13
ATION NUMBER: 60/276,703
; DATE: 2001-03-16
ATION NUMBER: 60/330,293
; DATE: 2001-10-18
ATION NUMBER: 60/322,127
; DATE: 2001-11-21
ATION NUMBER: 60/280,899
; DATE: 2001-04-02
ATION NUMBER: 60/310,797
; DATE: 2001-08-08
ATION NUMBER: 60/268,646
; DATE: 2001-02-14
or Application data removed - See File Wrapper or PALM.
Q ID NOS: 547
tentIn Ver. 2.1

artificial Sequence

NATION: Description of Artificial Sequence: PCR Primer
NATION: sequence

Q ID NOS: 547
tentIn Ver. 2.1
;

Artificial Sequence

IMATION: Description of Artificial Sequence: PCR Primer
IMATION: sequence
-482

milarity 52.1%; Score 14.6; DB 15; Length 22;
81.0%; Pred. No. 8.8e+03;
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

ATCATCTCTGCGATGTCAG 23
|||||
CTCATCTCTGCGATGTCAG 21

93
Application US/10098263B
o. US20030104410A1
MATION:
ittman, Michael
ENTION: Human Microarray
CE: 3118.1
ICATION NUMBER: US/10/098,263B
NG DATE: 2003-01-08
ATION NUMBER: 60/276,759
DATE: 2001-03-16
Q ID NOS: 131066
croarray Probe Sequence Listing Generator V 1.1

omo sapien
93

milarity 52.1%; Score 14.6; DB 14; Length 25;
81.0%; Pred. No. 8.9e+03;
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

GCATCATCTCTGCGATGTC 21
|||||
GCATCGCTCTGCGAAGGTC 24

94
Application US/10098263B
o. US20030104410A1
MATION:
ittman, Michael
ENTION: Human Microarray
CE: 3118.1
ICATION NUMBER: US/10/098,263B
NG DATE: 2003-01-08
ATION NUMBER: 60/276,759
DATE: 2001-03-16
Q ID NOS: 131066
croarray Probe Sequence Listing Generator V 1.1

omo sapien
94

milarity 52.1%; Score 14.6; DB 14; Length 25;
81.0%; Pred. No. 8.9e+03;
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 AGCATCATCTCTGCGATGTC 21
|||||
Db 4 AGCATCGCATCTGCAAGGTC 24

RESULT 26

US-09-904-099-22
; Sequence 22, Application US/09904099
; Publication No. US20030119092A1
; GENERAL INFORMATION:
; APPLICANT: Shankar, Geetha
; APPLICANT: Munning, Jason N
; APPLICANT: Spencer, Juliet V
; TITLE OF INVENTION: CHIMERIC G PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 10602-013-999
; CURRENT APPLICATION NUMBER: US/09/904,099
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence: Primer
; OTHER INFORMATION: Edg 5 receptors
US-09-904-099-22

Query Match 52.1%; Score 14.6; DB 10; Length 34;
Best Local Similarity 81.0%; Pred. No. 9.1e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0;

QY 6 CATCTCTGCGATGTCAGGTC 26
|||||
Db 1 CATCTACTGCGTCAAGTC 21

RESULT 27

US-09-904-099-23/c
; Sequence 23, Application US/09904099
; Publication No. US20030119092A1
; GENERAL INFORMATION:
; APPLICANT: Shankar, Geetha
; APPLICANT: Munning, Jason N
; APPLICANT: Spencer, Juliet V
; TITLE OF INVENTION: CHIMERIC G PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: 10602-013-999
; CURRENT APPLICATION NUMBER: US/09/904,099
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence: Primer f
; OTHER INFORMATION: Edg 5 receptors
US-09-904-099-23

Query Match 52.1%; Score 14.6; DB 10; Length 34;
Best Local Similarity 81.0%; Pred. No. 9.1e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0;

QY 6 CATCTCTGCGATGTCAGGTC 26
|||||
Db 34 CATCTACTGCGTCAAGTC 14

RESULT 28

US-10-418-182-89/c
; Sequence 89, Application US/10418182
; Publication No. US20030228302A1

```

: NUMBER OF SEQ ID NOS: 175
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 18
: LENGTH: 45
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Artificial
: OTHER INFORMATION: oligonucleotide sequence derived from multip
: OTHER INFORMATION: endothelial growth factor
US-09-795-006A-18

```

```
Query Match      52.1%; Score 14.6; DB 9; Length 45;
Best Local Similarity 81.0%; Pred. NO. 9.3e+03;
Matches 17; Conservative 0; Mismatches 4; Indels 0;
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RESULT 31

US-09-795-006A-9/c
; Sequence 9, Application US/09795006A
; Patent No. US20020151680A1

```

/ APPLICATION: A114140 EU A1
/
/ TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCU
/
/ TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAs AND PROTEINS
/
/ FILE REFERENCE: 28967/359778
/
/ CURRENT APPLICATION NUMBER: US/09/795,006A
/
/ CURRENT FILING DATE: 2001-02-26
/
/ PRIOR APPLICATION NUMBER: US 60/205,331
/
/ PRIOR FILING DATE: 2000-05-18
/
/ PRIOR APPLICATION NUMBER: US 60/185,205
/
/ PRIOR FILING DATE: 2000-02-25
/
/ NUMBER OF SEQ ID NOS: 175
/
/ SOFTWARE: Patentin Ver. 2.0
/

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```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Artificial
; OTHER INFORMATION: oligonucleotide sequence derived from multiple
; OTHER INFORMATION: endothelial growth factor
US-09-795-006A-9

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QY
5 TCATCCTCTGCATGGTCAGGT 25
45 TCATAATCTGCATGGTGATGT 25

RESULT 32
US-09-908-975-6030/c
; Sequence 6030, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASSERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Iiat
; APPLICANT: FAIGLER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TR
; TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; CURRENT FILING DATE: 2001-07-20
; PRIORITY APPLICATION NUMBER: US 60/287,724

DATE: 2001-05-02
ATION NUMBER: US 60/221,607
DATE: 2000-07-28
Q ID NOS: 32337
tentIn version 3.0
10

omo sapiens
1030

52.1%; Score 14.6; DB 10; Length 60;
milarity 81.0%; Pred. No. 9.5e+03;
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

GCATCATCTCTGCAGTGC 21
|||||
GCTTCATCTGTGCCAGTGC 27

8899/c

9, Application US/09908975
o. US20030165843A1

MATION:

HOSHAN, Avi

WASSERMAN, Alon

MINTZ, Eli

MINTZ, Liat

FAIGLER, Simchon

ENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE
ENTION: THAT POPULATE A TRANSCRIPTOME

CE: 36688-0005

ICATION NUMBER: US/09/908,975

NG DATE: 2001-07-20

ATION NUMBER: US 60/287,724

DATE: 2001-05-02

ATION NUMBER: US 60/221,607

DATE: 2000-07-28

Q ID NOS: 32337

tentIn version 3.0
99

omo sapiens

8899

52.1%; Score 14.6; DB 10; Length 60;
milarity 81.0%; Pred. No. 9.5e+03;
Conservative 0; Mismatches 4; Indels 0; Gaps 0;

TCTCTGCATGTCAGTGCAT 28
|||||
TTTCTCCAAGTTCAGTGCAT 30

10724/c

t, Application US/10098263B
o. US20030104410A1

MATION:

ttman, Michael

ENTION: Human Microarray

TE: 3118.1

ICATION NUMBER: US/10/098,263B

NG DATE: 2003-01-08

ATION NUMBER: 60/276,759

DATE: 2001-03-16

ID NOS: 131066

icroarray Probe Sequence Listing Generator V 1.1

14

ORGANISM: Homo sapien
US-10-098-263B-90724

Query Match 51.4%; Score 14.4; DB 14; Length 25;
Best Local Similarity 93.8%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 1; Indels 0

Qy 11 TCTGCATGTCAGTGC 26
|||||
Db 25 TCTGCATGTCAGTGC 10

RESULT 35

US-10-098-263B-109519

Sequence 109519, Application US/10098263B

Publication No. US20030104410A1

GENERAL INFORMATION:

APPLICANT: Mittman, Michael

TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 3118.1

CURRENT APPLICATION NUMBER: US/10/098,263B

CURRENT FILING DATE: 2003-01-08

PRIOR APPLICATION NUMBER: 60/276,759

PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 131066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 109519

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapien

US-10-098-263B-109519

Query Match 51.4%; Score 14.4; DB 14; Length 25;
Best Local Similarity 75.0%; Pred. No. 1.1e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0;

Qy 5 TCATCCTCTGCATGTCAGTGCAT 28
|||||
Db 2 TCTTCTCGCAGCCTCAGTGTGT 25

RESULT 36

US-09-944-411-14/c

Sequence 14, Application US/09944411

Patent No. US20020106799A1

GENERAL INFORMATION:

APPLICANT: FINER, MITCHELL H.

DULL, THOMAS J.

ZSEBO, KRISZTINA M.

COOKE, KEEGAN

FARSON, DEBORAH A.

TITLE OF INVENTION: METHOD FOR PRODUCTION OF HIGH TITER
VIRUS AND HIGH EFFICIENCY RETROVIRAL M
OF MAMMALIAN CELLS

NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:

ADDRESSEE: CELL GENESYS, INC.

STREET: 322 LAKESIDE DRIVE

CITY: FOSTER CITY

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/944,411

FILING DATE: 04-Sep-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/914,893

13 09:04:21 2004

us-10-090-326-23.max.rnpb

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FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/258,152
FILING DATE: 10-JUN-1994
APPLICATION NUMBER: US 08/076,299
FILING DATE: 11-JUN-1993
NEY/AGENT INFORMATION:
NAME: KRUPEN, KAREN I.
REGISTRATION NUMBER: 34,647
REFERENCE/DOCKET NUMBER: CELL 13.3
COMMUNICATION INFORMATION:
TELEPHONE: 415-358-9600 X131
TELEFAX: 415-349-7392
N FOR SEQ ID NO: 14:
NCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
ULE TYPE: DNA (genomic)
NCE DESCRIPTION: SEQ ID NO: 14:
14
51.4%; Score 14.4; DB 9; Length 26;
imilarity 75.0%; Pred. No. 1.1e+04;
; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

TCATCCTCTGCGATGTCAGTGCAT 28
|||||
TCACCTTCTTCAAGGTCAGATCTT 2

3/c
Application US/09759352
320020111474A1
FORMATION:
TANT: CAPON, DANIEL J
WEISS, ARTHUR
IRVING, BRYAN A
ROBERTS, MARGO R
ZSEBO, KRISTINA
OF INVENTION: CHIMERIC CHAINS FOR RECEPTOR-ASSOCIATED
SIGNAL TRANSDUCTION PATHWAYS
; OF SEQUENCES: 51
; ADDRESSEE: CELL GENESYS, INC.
; STREET: 322 LAKESIDE DRIVE
; CITY: FOSTER CITY
; STATE: CALIFORNIA
; COUNTRY: USA
; IP: 94404
; ER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; T APPLICATION DATA:
; APPLICATION NUMBER: US/09/759,352
; FILING DATE: 16-Jan-2001
; CLASSIFICATION: <Unknown>
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/567,393
; FILING DATE: 01-DEC-1995
; APPLICATION NUMBER: US 08/475,442
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/238,405
; FILING DATE: 05-MAY-1994
; APPLICATION NUMBER: US 07/988,194
; FILING DATE: 09-DEC-1992
; APPLICATION NUMBER: US 07/627,643
; FILING DATE: 13-DEC-1990
; APPLICATION NUMBER: WO PCT/US91/09431
; FILING DATE: 12-DEC-1991
```

```
ATTORNEY/AGENT INFORMATION:
NAME: KRUPEN, KAREN I.
REGISTRATION NUMBER: 34,647
REFERENCE/DOCKET NUMBER: CELL 5.13
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)358-9600 X131
TELEFAX: (415)349-7392
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-759-352-8
Query Match 51.4%; Score 14.4; DB 9; Length 26;
Best Local Similarity 75.0%; Pred. No. 1.1e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0

QY 5 TCATCCTCTGCGATGTCAGTGCAT 28
Db 25 TCACCTTCTTCAAGGTCAGATCTT 2

RESULT 38
US-10-147-299A-22/c
; Sequence 22, Application US/10147299A
; Publication No. US20040058323A1
; GENERAL INFORMATION:
; APPLICANT: KO, ALBERT I.
; APPLICANT: HAAKE, DAVID A.
; APPLICANT: REIS, MITERMAYER GALVAO
; APPLICANT: MATSUNAGA, JAMES
; APPLICANT: CRODA, JULIO HENRIQUE ROSA
; APPLICANT: SIQUEIRA, ISADORA CRISTINA
; APPLICANT: RILEY, LEE W.
; APPLICANT: BAROCCHI, MICHELE
; APPLICANT: YOUNG, TRACY ANN
; TITLE OF INVENTION: PROTEINS WITH REPETITIVE BACTERIAL-IG-LIKE
; FILE REFERENCE: 3673-19
; CURRENT FILING DATE: 2002-05-17
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-147-299A-22

Query Match 51.4%; Score 14.4; DB 12; Length 26;
Best Local Similarity 75.0%; Pred. No. 1.1e+04;
Matches 18; Conservative 0; Mismatches 6; Indels 0;

QY 4 ATCATCCTCTGCGATGTCAGTGCAT 27
Db 26 ATCATCCTCTGCGCTCTTGGAGTCA 3

RESULT 39
US-10-260-516-14/c
; Sequence 14, Application US/10260516
; Publication No. US20030199093A1
; GENERAL INFORMATION:
; APPLICANT: FINER, MITCHELL H.
; APPLICANT: DULL, THOMAS J.
; APPLICANT: ZSEBO, KRISTINA M.
; APPLICANT: COOKE, KEEGAN
```

3 09:04:21 2004

us-10-090-326-23.max.rnpb

FARSON, DEBORAH A.
OF INVENTION: METHOD FOR PRODUCTION OF HIGH TITER
VIRUS AND HIGH EFFICIENCY RETROVIRAL MEDIATED TRANSDUCTION
OF MAMMALIAN CELLS
OF SEQUENCES: 48
FUNDENCE ADDRESS:
DRESSEE: CELL GENESYS, INC.
TREET: 322 LAKESIDE DRIVE
ITY: FOSTER CITY
TATE: CALIFORNIA
COUNTRY: USA
IP: 94404
ER READABLE FORM:
EDIUM TYPE: Floppy disk
OMPUTER: IBM PC compatible
PERATING SYSTEM: PC-DOS/MS-DOS
FTWARE: Patentn Release #1.0, Version #1.25
T APPLICATION DATA:
PLICATION NUMBER: US/10/260,516
ILING DATE: 01-Oct-2002
LASSIFICATION: <Unknown>
APPLICATION DATA:
PLICATION NUMBER: US/08/914,893
ILING DATE: <Unknown>
PLICATION NUMBER: 08/517,488
ILING DATE: 21-AUG-1995
PLICATION NUMBER: US 08/258,152
ILING DATE: 10-JUN-1994
PLICATION NUMBER: US 08/076,299
ILING DATE: 11-JUN-1993
Y/AGENT INFORMATION:
AME: KRUPEN, KAREN I.
EGISTRATION NUMBER: 34,647
REFERENCE/DOCKET NUMBER: CELL 13.3
MUNICATION INFORMATION:
ELEPHONE: 415-358-9600 X131
ELEFAX: 415-349-7392
FOR SEQ ID NO: 14:
CE CHARACTERISTICS:
ENGTH: 26 base pairs
YPE: nucleic acid
RANDEDNESS: single
POLOGY: linear
LE TYPE: DNA (genomic)
CE DESCRIPTION: SEQ ID NO: 14:
4
51.4%; Score 14.4; DB 14; Length 26;
milarity 75.0%; Pred. No. 1.1e+04;
Conservative 0; Mismatches 6; Indels 0; Gaps 0;
TATCCTCTGCATGTCAGTGCAT 28
TACCTTCTCAAGGTCAGATCTT 2
10
Application US/09801274
20020032319A1
ATION:
rgill, Michele
reland, James S.
ander, Eric S.
ENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
E: 2825.2009-001
ICATION NUMBER: US/09/801,274
NG DATE: 2001-03-07
ATION NUMBER: US 60/187,510
DATE: 2000-03-07
ATION NUMBER: US 60/206,129
DATE: 2000-05-22
ID NOS: 1802

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 130
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-801-274-130
Query Match 51.4%; Score 14.4; DB 9; Length 31;
Best local Similarity 83.3%; Pred. No. 1.1e+04;
Matches 15; Conservative 1; Mismatches 2; Indels 0.
Qy 3 CATCATCCTCTGCATGCT 20
Db 12 CATCTCCTCTCCATGCT 29
Search completed: April 12, 2004, 21:42:57
Job time : 143.308 secs